GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model 1 OM protein 5, 2004, 14:30:20 ; Search time 127:123 Seconds (without alignments) 568.992 Million cell updates/sec May Run on:

US-10-067-122B-2 1428 1 MGNNCYNVVVIVLLLVGCEK......DACSCRCPQEEEGGGGGYEL 256 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

1586107 seqs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Listing first 45 summaries

geneseqp1980s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

Kles	Description	Aar64199 Murine 4	Aar70978 4-1BB rec	417		Aay28687	Aay332	Aae22581	Abb75954	Adc25	Ade87549	Aab66986 41bb pro	Aar64197	77 H4-1BB	, Aaw26658	Aay28688 Human	Aay33214 Human	. Aae0854	Aab50521 Human	Abb7595	Abr39863 Human	Abb8464	Aae39531 Human p	Adc78803 Human PR	Add25599	Adeed2541 Timbroum
SUMMARIES	ID	AAR64199	AAR70978	AAW04173	AAW26659	AAY28687	н	AAE22581	ABB75954	ADC25939	ADE87549	AAB66986	19	AAR70977	AAW26658	AAY28688	AAY33214	AAE08546	AAB50521	ABB75955	ABR39863	ABB84640	AAE39531	ADC78803	ADD25599	1700004
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ALIGNMENTS

T-cell; lymphocyte; activation; tissue culture; clone; cell lines; proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine. AAR64199 standard; protein; 256 AA (revised)
(first entry) Murine 4-1BB polypeptide. 25-MAR-2003 08-AUG-1995 AAR64199; RESULT 1
AAR64199
ID AAR6
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AAC AAR6
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DT 25-M
DT 08-A
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Mus musculus. WO9426290-A1.

94WO-US005036. 06-MAY-1994; 24-NOV-1994.

93US-00060843. (IMMV) IMMUNEX CORP. 07-MAY-1993;

Smith CA, Goodwin RG,

Alderson MR;

WPI; 1995-022265/03. N-PSDB; AAQ75428.

Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB to transduce signal.

Example 1; Page 44-45; 65pp; English.

The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422) are useful in a pharmaceutical composition for stimulating the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring mechanisms of T-cell activation, as they are expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It may also be used to stimulate proliferation of activated T-cells, used in therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 256 AA;

Query Match

100.0%; Score 1428; DB 2; Length 256;

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08:16:48 2004

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Length 256;

DB 2;

Score 1428;

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Sequence 256 AA;

Query Match

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                                                                                                                                                              cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was isolated using PCR primers based on the homologous mouse 4-1BB gene (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel cDNA encoding human receptor protein H4-1BB - useful to produce the protein which is used to treat auto:immune disease and facilitate organ
                                                1 MGNNCYNVVIVILLVGCEKVGAVQNSCDNCQPGTPCRKYNPVCKSCPPSTFSSIGGQPN
                                                                     CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                               LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG
                               1 MGNNCYNVVVIVILLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
             Gaps
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             Indels
   red. No. 1.7e-109;
Mismatches 0;
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/label= Sig_peptide
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                                                                                                                                                                                                                                                           AAR70978 standard; protein; 256 AA.
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Best Local Similarity 100.0%; P
Matches 256; Conservative 0;
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(first entry)
                                                                                                                                                                                                                                                                                                                              4-1BB receptor protein.
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N-PSDB; AAQ86127.
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16-OCT-1995
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody specific for human receptor protein 4\text{-}1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating auto:immune diseases
                                                                                                                                                                                                                            121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG
                                                                                                                                                                                                                                                                                                     181 GHSLQVLTLFLALTSALLLALIFITILFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell; immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
                                                                                  1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                                              CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                                                         CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
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                                                      1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
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Best Local Similarity 100.0%; Pred. No. 1.7e-109; Matches 256; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04173 standard; protein; 256 AA.
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N-PSDB; AAT39541.
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Sequence 256 AA;

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This protein comprises mouse 4-1BB, a member of the tumour necrosis factor receptor superfamily that is expressed on helper, suppressor and cytolytic T cells, as well as on mouse brain tissue. A novel claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned and sequenced (see AAW26656) that binds to murine 4-1BB. 4-1BB-L, especially its soluble extracellular domain, can be used to stimulate T-cell proliferation in vitro, as a research tool and as an affinity ligand for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                  DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell; proliferation; immunostimulant.
                                                                    1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                               CNICRVCAGYPRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                                                  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG
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                                                                                                                                                                                                 GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS
                                               1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                      Gaps
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         red. No. 1.7e-109;
Mismatches 0;
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          Pred.
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                        256; Conservative
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           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1994;
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25-FEB-1998
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The present sequence is mouse 4-1BB receptor protein. This protein has 65% homology with human receptor protein 4-1BB. The protein has a putative leader sequence, a potential membrane anchor segment and other features of known receptor proteins. 4-1BB is structurally related to members of the nerve growth factor receptor. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation;
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                                                                                1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                                                                                                     LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTT1SVTPEGGPG
                                                                                                                                                                                                                121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG
                                                                                                                                                                                                                                                                  181 GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS
                                                                                                                                                      CNICRVCAGYPRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                          CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
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                                                             1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
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 Length 256;
                                Indels
100.0%; Score 1428; DB 2;
100.0%; Pred. No. 1.7e-109;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
   Query Match
Best Local Similarity 100.
Matches 256; Conservative
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Mellitus, Rheumatoid
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for activation or inhibition of immune response; to block H4-1BB ligand binding; treating cancerous tumours and autoimmune diseases; and during organ transplantation
                                                                                                                                                      1 MGNNCYNVVVIVLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                                                        1 MGNNCYNVVVIVILLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                                                                                                                                     61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                                                                                                                                                                            LGTFNDQNGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPP
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                                                                                                                 Gaps
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0
                                                                                      Length 256;
                                                                                                              Indels
                                                                                100.0%; Score 1428; DB 2;
100.0%; Pred. No. 1.7e-109;
ive 0; Mismatches 0;
                                                                                   100.0%; Fr.
0;
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                                                                                               Best Local Similarity 100.
Matches 256; Conservative
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                                                      Sequence 256
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                                                                                 Query Match
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    AAY33215 standard; protein; 256
            18-NOV-1999 (first entry)
                Murine CD137 protein
        AAY33215;
                                    Mus sp
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fungal; CD137; monocyte growth factor; proliferation; peripheral monocyte; treatment; disease; antitumor; antibacterial; antiviral; antifungal; immunostimulatory; non-specific immune response; phagocytosis; intracellular destruction; microorganism; immune complex; antibody; cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia; chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal bacterial; viral infection; immunosuppressant; gene therapy; murine.

WO9944629-A2

10-SEP-1999

99WO-EP001440 05-MAR-1999;

98EP-00103859 05-MAR-1998;

(MERC) MERCKLE GMBH.

Langstein J;

Schwarz H,

WPI; 1999-550983/46.

Use of monocyte growth factor CD137 for stimulating proliferation of peripheral monocytes, particularly for treating immune deficiency, e.g. following cancer therapy

Disclosure; Fig 1B; 57pp; German.

This invention describes a novel use of the human monocyte growth factor CD137, or its functional analogs, for (i) stimulating proliferation of

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peripheral monocytes; and (ii) treating diseases that are associated with disorders of a cellular system that includes monocytes (and/or their disorders of a cellular system that includes monocytes (and/or their progression is treatable by stimulating proliferation of such cells. The products of the invention have antitumor, antiboacterial, antiviral, antifungal and immunostimulatory activity. Stimulating proliferation of monocytes promotes the non-specific immune response, i.e. it increases phagocytosis and intracellular destruction of microorganisms, immune cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat diseases associated with a defective immune response where caused by inadequate numbers of active monocytes/macrophages, especially damage to therapy; disorders of wound healing (e.g. in dialysis or diabetic therapy; disorders of wound healing (e.g. in dialysis or diabetic patients, or those with chronic venous insufficiency); tumors; bacterial, fungal or viral infections; (non-)congenital or (non-)inherited diseases or injury to the immune system; injury induced by treatment with disease, or transplant patients with chronic arthritis or autoimmune confinency in gene therapy procedures. Proliferation of peripheral monocytes is achieved independently of hematopoietic stem cells. This sequence represents the murine CD137 protein described in the method of the invention
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/label= Signal_peptide
23. .256
/note= "Mature receptor 4-1BB protein"
128. .130
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100.0%; Pred. No. 1.7e-109;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 256; Conservative
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MIP-1alpha; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 256 AA;
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AC AAE2

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DE MOUE

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XW MIP-

KW 4-1E

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OS MUS

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FH Key

FT Pept

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS 240
                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated and purified cDNA containing mouse lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by which the immune cells communicate with each other. Lymphokines are used therapeutically against immunologic diseases. Mouse lymphokine MIP-alpha can be used to modulate early myeloid progenitor cell differentiation. The present sequence is mouse lymphokine receptor 4-1BB protein
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100.0%; Pred. No. 1.7e-109;
iive 0; Mismatches 0;
 /note= "Asn is N-glycosylated"
138. .140
/note= "Asn is N-glycosylated"
                                                                                                                                                                     (ADRE-) ADVANCED RES & TECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 3; 81pp; English
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                                                                                                               92US-00922996
                                                                                                                                          88US-00267577
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Matches 256; Conservative
                                                                                                                                                                                                  Kwon BS, Broxmeyer HE;
                                                                                                                                                                                                                          WPI; 2002-370577/40.
N-PSDB; AAD35694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 256 AA;
                Modified-site
                                                                                                               30-JUL-1992;
                                                                                                                                           07-NOV-1988;
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The present sequence is the protein sequence of the murine cytokine receptor, 4-1BB. A portion of the extracellular (ligand binding) domain of the receptor was utilised in a murine 4-1BB/human 1gG1 Fc fusion protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see ABB75952). The invention provides novel murine and human 4-1BB-L polypeptides and human 4-1BB polypeptides, as well as DNA sequences encoding them, recombinant expression vectors and host cells, and methods for producing the novel polypeptides by cultivating the transformed host cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from their extracellular domains, have therapeutic value. Antibodies that are immunoreactive with 4-1BB-L or human 4-1BB are claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody specific for the cytokine 4-1BB-ligand, useful immunoaffinity purification of the ligand.
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100.0%; Pred. No. 1.7e-109;
iive 0; Mismatches 0;
                         1. .23
/label= Signal_peptide
24. .256
/label= Mature_protein
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Location/Qualifiers
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94US-00236918.
97US-00910449.
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nes 256; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             (IMMV) IMMUNEX CORP
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06-MAY-1994;
05-AUG-1997;
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       Key
Peptide
                                                                         Protein
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The invention relates to a novel cDNA gene encoding receptor protein 4-18B. The CDNA gene of the invention demonstrates immunostimulant activities and may be useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein encoded by the DNA. The protein, its fragments and derivatives may be useful as a probe to isolate ligands to receptor protein 4-18B, for stimulating proliferation of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand binding. The antibody may be useful for enhancing T-cell proliferation or activation. Finally, the invention may be useful with respect to cancer research. The current sequence is that of the murine receptor 4-1BB
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                                                                                                                                                         immunostimulant; B-cell activation; T-cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
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100.0%; Pred. No. 1.7e-109;
ative 0; Mismatches 0;
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92US-00922996.
93US-00012269.
                                                                                            Murine receptor 4-1BB protein.
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                                                                                                                                                         receptor 4-1BB; immuncancer; murine; mouse
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N-PSDB; ADC25938.
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01-FEB-1993;
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                                                                                                                                       immunosuppressive, H4-1BB ligand binding blocker, mouse, receptor protein; H4-1BB, B-cell proliferation stimulator; T-cell proliferation enhancer; immune system supressor; transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cDNA, or its encoded receptor protein H4-1BB, useful as probes to isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking H4-1BB ligand binding to facilitate organ transplantation or treat
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100.0%; Pred. No. 1.7e-109;
tive 0; Mismatches 0;
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              standard; protein; 256
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92US-00922996.
93US-00012269.
95US-00460976.
97US-00955573.
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Best Local Similarity 100.
Matches 256; Conservative
                                                                                                          Mouse receptor H4-1BB.
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N-PSDB; ADE87548.
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30-JUL-1992;
01-FEB-1993;
05-JUN-1995;
22-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.
                                                                                                                                                                                                                                                              Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.
   240
                 181 GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS 240
   CHSLOVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEEDACS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calzone FJ,
                                                                                                                                                        AAB66986 standard; protein; 191
                                                          CRCPOEEEGGGGGYEL 256
                                                                                    241 ČŘCPÓŠEEGGGGGÝEĽ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00350670.
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                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lacey DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-103031/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200103719-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1999;
                                                                                                                                                                                                                                         41bb protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1999;
                                                                                                                                                                                                              19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2001
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                                                           241
                                                                                                                                                                                    AAB66986;
      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boyle
                                                                                                                            RESULT 11
AAB66986
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The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423) are useful in a pharmaceutical composition for stimulating the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring mechanisms of T-cell activation, as they are expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It may also be used to stimulate proliferation of activated T-cells, used in therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                           121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                               120
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                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        okine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB transduce signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                              1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                               1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                                                                                                  LGTPNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell; lymphocyte; activation; tissue culture; clone; cell lines; proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
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Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÄR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 39; Page 47-48; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR64197 standard; protein; 255 AA.
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(first entry)
                                                                                                                                                                                                                                                                                                         CHSLOVLTLFL 191
                                                                                                                                                                                                                                                                                                                                                         GHSLQVLTLFL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 4-1BB polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-022265/03.
N-PSDB; AAQ75424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9426290-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR64197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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Length 191;

Score 1085; DB 4; Pred. No. 2.1e-81;

76.0%; S

Query Match Best Local Similarity

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120
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                                                                                                                        120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                       178 AREPGHSPQIISFFLALTSTALLFLTLRFSVVKRGRKKLLYIFKQPFWRPVQTTQE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using probes based on the mouse receptor protein 4-1BB gene. The PCR product was used to screen a cDNA library of activated human T-cells. The isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel cDNA encoding human receptor protein H4-1BB - useful to produce the protein which is used to treat auto:immune disease and facilitate organ transplantation.
                                    121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
                                                                                                                                                                                                                                             180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQE
60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H4-1BB; receptor protein; immunosuppressive; autoimmune disease; organ transplantation; cell membrane ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70977 standard; protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 2; 36pp; English.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H4-1BB receptor protein
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N-PSDB; AAQ86126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09507984-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1995.
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16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                             236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
AAR70977
ID AAR70
XX
DT 25-MA
DT 16-OC
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DT 16-OC
XX
DT 16-OC
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DE H4-1E
XW
OS HOMO
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OS HOMO
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177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This protein comprises human 4-1BB, a member of the tumour necrosis factor receptor superfamily that is expressed on cells that include, but are not limited to, stimulated human peripheral blood lymphocytes. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT91026) obtained from human peripheral blood T-lymphocytes. A novel claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L,
                                                                                                                                                                                                                                                                                                            4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell; proliferation; immunostimulant.
                                                   121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
                                                                                               120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
                                                                                180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187. .213
/label= Transmembrane
214. .255
/label= Extracellular
                                                                                                                                                                                                                                                                                                                                                                                    .. .23
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                        iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Col 43-44; 32pp; English
                                                                                                                                                                                                           AAW26658 standard; protein; 255 AA.
                                                                                                                                         238 EDGCSCRFPEEEEGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00236918
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(first entry)
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/label= Cy
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                                                                                                                             236 EDACSCRCPQEEEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                               115. .117
                                                                                                                                                                                                                                                                                          Human 4-1BB receptor,
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-1993;
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25-FEB-1998
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                                                                                                                                                                                                                                 AAW26658;
                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                     RESULT 14
AAW26658
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60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119

55.7%; Score 795; DB 2; Length 255; 58.4%; Pred. No. 2.1e-57; iive 31; Mismatches 67; Indels

Conservative

Similarity

Query Match Best Local Simi Matches 149;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
especially its soluble extracellular domain, can be used to stimulate T-cell proliferation in vitro, as a research tool and as an affinity ligand for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation; mouse 4-1BB cDNA; monoclonal antibody; immune response; organ transplantation; autoimmune disease; diabetes; cancerous tumour; rheumatoid arthritis; lupus; nerve growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                   60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTPBGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                                             1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 4-1BB ligands to, e.g. treat Diabetes Arthritis and Systemic Lupus Erythematosus.
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&
                                                                                                                                                                                              55.7%; Score 795; DB 2; Length 255; 58.4%; Pred. No. 2.1e-57; ive 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18. .255
/note= "Purified human 4-1BB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY28688 standard; protein; 255 AA
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                                                                                                                                                                                                    Query Match
Best Local Similarity 58.49
Matches 149; Conservative
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Mellitus, Rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-444325/37.
N-PSDB; AAZ08961.
                                                                                                                                       Sequence 255 AA
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AAY28688
ID AAY2
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AC AAY2
XX
AC AAY2
XX
DE Huma
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COS Home

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The present sequence is a human receptor protein 4-1BB. 4-1BB is structurally related to members of the nerve growth factor receptor. It contains a putative zinc finger structure similar to that of yeast e1F-2b protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation; B cell proliferation; treating cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand binding has practical application in the suppression of immune system during organ transplantation or against autoimmune diseases including diabetes, rheumatoid arthritis, and lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NCNICRVCAGYFREKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.7%; Score 795; DB 2; Length 255; Best Local Similarity 58.4%; Pred. No. 2.1e-57; Matches 149; Conservative 31; Mismatches 67; Indels
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N-PSDB; AAZ09769.
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                                                                                                                                                                                                                                                                                                                                                               Seguence 255 AA;
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This invention describes a novel use of the human monocyte growth factor CD137, or its functional analogs, for (i) stimulating proliferation of peripheral monocytes; and (ii) treating diseases that are associated with calsorders of a cellular system that includes monocytes (and/or their derived cells, precursor or progenitors) or where the origin and/or progression is treatable by stimulating proliferation of such cells. The products of the invention have antitumor, antibacterial, antiviral, antifungal and immunostimulatory activity. Stimulating proliferation of monocytes promotes the non-specific immune response, i.e. it increases thangocytesis and intracellular destruction of microorganisms, immune complexes and damaged cells, and improves antibody (in) dependent cytotoxicity to tumor cells, and improves antibody (in) dependent cytotoxicity to tumor cells, and improves antibody (in) dependent cytotoxicity to tumor cells, cD137 is used, in vivo or ex vivo, to treat consequate numbers of active monocytes/macrophages, especially damage to the hematopoietic system (leucopenia) caused by chemotherapy or radiation therapy; disorders of wound healing (e.g. in dialysis or diaberic patients, or those with chronic venous insufficiency); tumors; bacterial, fungal or viral infections; (non-)congenital or (non-)inherited diseases or injury to the immune system; injury induced by treatment with immune system; injury induced by treatment with cimmunesuppressants (e.g. patients with chronic activities or autoimmune consense represents the human CD137 protein described in the method of the invention
                            Use of monocyte growth factor CD137 for stimulating proliferation of peripheral monocytes, particularly for treating immune deficiency, e.following cancer therapy.
                                                                                                                                         Claim 12; Fig 1A; 57pp; German.
                            Use of mono
peripheral
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Sequence 255 AA;

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60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEXDCRPGQELTKQGCKTC 119
                                                                                                                                                                              61 TCDICROCKGVFRTRKECSSTSNABCDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC 120
                                                                                                                                                                                                                           120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                                121 CFGTFNDOK-RGICRPWINCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
                                                                                                                   9
                                                                                                 AREPGHSPQIISFFLALTSTALLFFLTLFFSVVKRGRKKLLYIFKQPFWRPVQTTQE
                                                                           1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
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55.7%; Score 795; DB 2; Length 255; 58.4%; Pred. No. 2.1e-57; rative 31; Mismatches 67; Indels
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                     Best Local Similarity 58.49
Matches 149; Conservative
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   Query Match
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AAE08546; RESULT 17 AAE08546
ID AAE0
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AC AAE0
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DT 15-N
XX
DE Huma
XX
KW Huma
KW Huma
KW Wunn

AAE08546 standard; protein; 255 AA.

15-NOV-2001

Human h4-1BB receptor.

Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour; tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock; wound healing; autoimmune disease; acquired immunedeficiency syndrome;

AIDS; graft-host rejection; cellular proliferation; cerebral malaria; bone resorption; human immunodeficiency virus; HIV; graft rejection; inflammation; antibacterial; immunosuppressive; vulnerary; vasotropic; antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.

JS2001014465-A1

16-AUG-2001

L9-DEC-2000; 2000US-00739394.

96US-0013474P. 97US-00816605. 99US-00253549. 15-MAR-1996; 13-MAR-1997; 22-FEB-1999;

(NIJJ/) NI J. (YUGG/) YU G. (GENT/) GENTZ R. (DILL/) DILLON P J.

Dillon PJ; Gentz R, Yu G,

WPI; 2001-529104/58

treatment New human 4-1BB receptor splicing variant polypeptides and polynucleotides, useful for research, diagnosis, prevention and treatmen of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency syndrome and graft rejection.

Disclosure; Fig 2; 28pp; English.

The present invention relates to an isolated human 4-1BB receptor
splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
gene therapy. h4-1BBSV is useful for research, biological, clinical and
therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
are useful as an immunogen to produce antibodies which are useful for
isolating and identifying clones expressing the polypeptide or to purify
the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
disorders of cells, tissues and organisms and its nucleic acid is useful
complementary polynucleotides for e.g. as a diagnostic
for detecting complementary polynucleotides for e.g. as a diagnostic
creagent and for chromosomal identification. h4-1BBSV receptor agonists
are useful for preventing, treating tumours, restenosis, cytotoxicity,
autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graftbacterial and viral infection, deleterations effects of ionising radiation,
autoimmune diseases, acquired immune responses, wound healing and cellular
coliferation and antagonists are useful for treating and/or preventing
endotoxic shock, inflammation, cerebral malaria, activation of human
immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
immunodeficiency virus (HIV) virus, bone resorption, graft rejection and

Sequence 255 AA;

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119 120 179 235 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177 9 180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE 60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP Gaps .; 8 Length 255; 67; Indels Query Match 55.7%; Score 795; DB 4; Best Local Similarity 58.4%; Pred. No. 2.1e-57; Matches 149; Conservative 31; Mismatches 67;

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The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic, antiparasitic, cardiant, antiniflammatory, anticonvulsant, antiparasitic, cardiant, anti-HV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and parasite, bacteria and viruses, restenosis and graft versus host disease. Comparasity are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by consist or TRAIL binding facilitator. The antibodies which bind TRID colympeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death, The TRID colympletides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison of the present invention
178 AREPGHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cancer; cardiovascular disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.
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                                                                                    EDACSCRCPOEEEGG 250
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200071150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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AAB50521
ID AAB50
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AAC AAB50
DE T15-MA
XXX
THUMAN
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Gaps

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Query Match 55.7%; Score 795; DB 4; Length 255; Best Local Similarity 58.4%; Pred. No. 2.1e-57; Matches 149; Conservative 31; Mismatches 67; Indels

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60 NCNICRVCAGYFREKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC

1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP

120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179 180 G---GHSLQVLTLFLALTS-ALLLALIFITILFSVLKWIRKKFPHIFKQPFKKTTGAAQE 235

250

EDACSCRCPOREEGG

236

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for
                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody specific for the cytokine 4-1BB-ligand, useful
                                                                                                                                                                                    24. .186
/note= "extracellular domain"
138. .140
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                    149. .151
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                     /note= "transmembrane region" 214. .255
                                                                                                                                                                                                                                                            /note= "cytoplasmic domain"
                                                                                                                                                                     4. .255
label= Mature_protein
                                                                                                                                                      . .23
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                             Alderson MR
                                                                                                                                            Location/Qualifiers
                                             ABB75955 standard; protein; 255 AA
                                                                                                             Cytokine; receptor; 4-1BB; human
                                                                                                                                                                                                                                                                                                                            93US-00060843.
94US-00236918.
97US-00910449.
                                                                                            Human cytokine receptor 4-1BB.
                                                                                                                                                                                                                                                                                                             98US-00150864.
238 EDGCSCRFPEEEEGG 252
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Goodwin RG, Smith CA,
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-380940/41.
N-PSDB; ABL54048.
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                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                     Modified-site
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06-MAY-1994;
05-AUG-1997;
                                                                                                                                                                                                                                                                              US6355779-B1
                                                                                                                                                                                                                                                                                                              10-SEP-1998;
                                                                              12-JUL-2002
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                               12-MAR-2002
                                                              ABB75955;
                                                                                                                                               Key
Peptide
                                                                                                                                                                      Protein
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                                                                                                                                                                                      Domain
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Sequence 255 AA;

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ABB84640 standard; protein; 255 AA.
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                                                                                                                                              Lucas J, Dialynas D,
                                                                                                                                                                        WPI; 2003-268084/26.
                                                                                                                     (GEST ) GENSET SA
                                                                                                                                                                                      N-PSDB; ACC47324
                  WO2003011325-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 255 AA;
                                           13-FEB-2003
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ABB84640
ID ABB84
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AC ABB84
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DT 05-FE
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                                             The present sequence is the protein sequence of the human cytokine receptor, 4-1BB. The sequence was deduced from a cDNA clone (see ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion of the extracellular (ligand binding) domain of the human 4-1BB cytokine receptor was utilised in a human 4-1BB/human IgG1 Fc fusion protein, which was used to identify the human 4-1BB ligand (4-1BB-L, see ABB75953). The invention provides novel murine and human 4-1BB-L polypeptides, as well as DNA sequences encoding them, recombinant expression vectors and host cells, and methods for producing the novel polypeptides by cultivating the transformed host cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from their extracellular domains, have therapeutic value. Antibodies that are immunoreactive with 4-1BB-L or human 4-1BB are claimed
                                                                                                                                                                                                                                                                                                                                                                        60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119
                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                        61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AREPGHSPQIISFFLALTSTALLFFLTFFLTRFSVVKRGRKKLLYIFKQPFWRPVQTTQE
                                                                                                                                                                                                                                                                                                                        1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLXWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic; antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective; hypotensive; immunomodulator; antidepressant; human; receptor.
                                                                                                                                                                                                                                                                     55.7%; Score 795; DB 5; Length 255; 58.4%; Pred. No. 2.1e-57; Live 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "extracellular domain"
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immunoaffinity purification of the ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "mature protein'
                         Example 2; Col 43-44; 31pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDGCSCRFPEEEEGG 252
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214. .255
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Best Local Similarity 58.4
Matches 149; Conservative
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/note= "m
18. .186
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187. .21
                                                                                                                                                                                                                                              Sequence 255 AA;
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Peptide
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ABR39863
XX
XC ABR39
XX
DT 11-AU
XX
DE Human
XX
W MOCEP
XW ANLII
XW ANLII
XW ANLII
XW ANLII
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The invention relates to an agonist or antagonist of MOCEPTIN (a member of the Tumour Necrosis Factor Receptor family) activity. The antagonist or agonist of MOCEPTIN activity, or the composition comprising the agonist or antagonist, is useful for preventing or treating an obesity-related disorder or disease in an individual. In particular, the agonist of MOCEPTIN activity is useful for treating or preventing obesity-related diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance, diabetes, stroke or hypertension. The agonist is also useful for reducing body mass, or for treating or preventing disorders associated with excessive weight loss, e.g. preventing disorders associated with excessive weight loss, c.g. cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease-related weight loss, or anorexia. The present sequence represents a human MOCEPTIN polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                      New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis Factor Receptor family) activity, useful for preventing or treating obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CFGTFNDQK-RGICRPWINCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
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25-JUL-2002; 2002WO-IB003499.
                                                                           27-JUL-2001; 2001US-0308142P
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This invention describes a novel human h4-1BBSV receptor or a sequence that is at least 85% identical to the h4-1BBSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, antiinflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to a disease related to underexpression of h4-1BBSV or for identifying a disease related to underexpression of h4-1BBSV or for identifying a disease related to underexpression of th4-1BBSV or for identifying a disease or susceptibility to a consists and antagonists. The soluble extracellular domain of h4-1BBSV receptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human cachexia, tumours, autoimmune disease, ionizing radiation, acquired immunodeficiency syndrome (AIDS), for providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells and certain haematopoietic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist. This sequence represents the human 4-1BB receptor described in the anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator; vasotropic; gene therapy; chromosome mapping; extracellular domain; endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease; human immunodeficiency virus; HIV; graft-host rejection; bone resorption; cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome; AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis; autoimmune disease; h4-1BB. Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors, providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis. h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive, Dillon PJ; Disclosure; Fig 2; 29pp; English 15-MAR-1996; 96US-0013474P. 13-MAR-1997; 97US-00816605. 22-FEB-1999; 99US-00253549. 19-DEC-2000; 2000US-00739394. (HUMA-) HUMAN GENOME SCI INC. 2002US-00097330 disclosure of the invention Gentz RL, receptor WPI; 2003-066900/06. US2002127651-A1 Yu G, 15-MAR-2002; Homo sapiens 12-SEP-2002 n, Human; Human

S S 9 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTPC-RKYNPVCKSCPPSTFSSIGGQP .. 00 Query Match 55.7%; Score 795; DB 6; Length 255; Best Local Similarity 58.4%; Pred. No. 2.1e-57; Matches 149; Conservative 31; Mismatches 67; Indels 57; 67; Indels Sequence 255 AA;

120 60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119 CFGIFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177 61 TCDICROCKGVFRTRKECSSTSNARCDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC 120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 121 셤 원 δ ઠે 8

9 60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119 120 The invention relates to a method and apparatus for applying adhesive to packaging in a variety of configurations. The method involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction. The invention is useful for e.g. soap boxes, cereal boxes, bottle carriers, can boxes. The present sequence is human protein. Note: There is no specific information about the sequence in the specification 9 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP Paper board container manufacture for soap boxes, involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to 8; Gaps Length 255; Query Match
Best Local Similarity 58.4%; Pred. No. 2.1e-57;
Matches 149; Conservative 31; Mismatches 67; Indels /note= "Encoded by AGA" Disclosure; Page 12-13; 46pp; English. Location/Qualifiers 107 AAE39531 standard; protein; 255 AA 08-JUN-2001; 2001US-00877336 08-JUN-2001; 2001US-00877336 Human protein SEQ ID NO: 2. Human; adhesive; packaging Walsh JC, Hawkins KE; WPI; 2003-266968/26. N-PSDB; AAD59981. ω. (WALS/) WALSH J C. (HAWK/) HAWKINS K another direction. Sequence 255 AA; Misc-difference US2003000851-A1 Homo sapiens 02-JAN-2003. 18-DEC-2003 AAE39531; 236 AAE39531 g ð g ਨੇ ठ

235

G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE

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                                                                     AREPGHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237
120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                       235
                      121 CFGTFNDOK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises the amino acid and coding sequences of human PRO proteins. The DNA and protein sequences of the invention are useful for the diagnosis and treatment of cancer and inflammatory bowel disease (e.g. ulcerative colitis or Crohn's disease). The present amino acid sequence represents a human PRO protein of the invention.
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                                                 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polynucleotide and polypeptide, useful for the manufacture of medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.
                                                                                                                                                                                                                                                                                                                  PRO; cancer; inflammatory bowel disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
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58.4%; Pred. No. 2.1e-57;
ative 31; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; SEQ ID NO 32; 327pp; English.
                                                                                                                                                                                                     ADC78803 standard; protein; 255 AA.
                                                                                                                        238 EDGCSCRFPEEEEGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2002; 2002WO-US033070.
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                                                                                                         EDACSCRCPQEEEGG 250
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                    Human PRO protein #16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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N-PSDB; ADC78802.
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Best Local Similarity
Matches 149; Conserv
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                                                                                                                                                                                                                                                                                                                             Crohn's disease
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the CH2 constant region polypeptide. The instance of the CH2 constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypement for an encomplement fixation.
 235
                                           237
                                                                                                                                                                                                                                                                                                                                                                                                 Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                        180 G---GHSLOVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                                                                                                                                                                                             Binding domain-immunoglobulin fusion protein-associated protein #77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 160; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ledbetter JA, Hayden-Ledbetter MS,
                                                                                                                                                                                                                                 ADD25599 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-2002; 2002US-00207655.
                                                                                                                         238 EDGĆŚĆRFPEEEEĠĠ 252
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                    236 EDACSCRCPQEEEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENECRAFT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-801317/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2003.
                                                                                                                                                                                                                                                                         ADD25599;
                                                                                                                                                                                          RESULT 24
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Gaps

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60 NCNICRVCAGYFREKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119

61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC

g ò g ò

1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP

Conservative

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antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain limunoglobulin fusion protein-associated protein sequence or the sequence. Note: The sequence at a for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NCNICRVCAGYFREKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; H4-1BB ligand binding blocker; human;
receptor protein; H4-1BB; B-cell proliferation stimulator;
T-cell proliferation enhancer; immune system supressor; transplantation;
autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCDICROCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  55.7%; Score 795; DB 7; Length 255; 58.4%; Pred. No. 2.1e-57; Indels iive 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE87541 standard; protein; 255 AA
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92US-00922996.
93US-00012269.
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EDGCSCRFPEEEEGG 252
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Best Local Similarity 58.49
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                      Sequence 255 AA;
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30-JUL-1992;
01-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119
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                                                                                                                                              New cDNA, or its encoded receptor protein H4-1BB, useful as probes to isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking H4-1BB ligand binding to facilitate organ transplantation or treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.7%; Score 795; DB 7; Best Local Similarity 58.4%; Pred. No. 2.1e-57; Matches 149; Conservative 31; Mismatches 67;
                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04174 standard; protein; 255 AA.
95US-00460976.
97US-00955573.
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                                                                                                        WPI; 2003-576599/54.
N-PSDB; ADE87540.
                                                                                                                                                                                                   autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 255 AA;
                                            (KWON/) KWON B
05-JUN-1995;
22-OCT-1997;
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                                                                          Kwon BS;
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                                                                                                                                                              Monoclonal antibody specific for human receptor protein 4-1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating auto:immune diseases.
                                                                                                                                                                                                                             Novel human receptor protein H4-1BB (AAW04174) has the potential to function as an accessory signaling molecule during T-cell activation and proliferation. Its amino acid sequence was deduced from a cDNA clone (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-1BB can be produced in transfected host cells. It is used to isolate receptor ligands, to stimulate B-cells expressing such ligands and to block H4-1BB ligand binding. A fusion protein of H4-1BB with human placental alkaline phosphatase can be used to modify immune responses. A monoclonal antibody raised against an immunoepitope (see also AAW04172) of H4-1BB is useful in the treatment of cancer and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILA; receptor inducible by lymphocyte activation; disease diagnosis; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                           Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                         54.8%; Score 782; DB 2;
58.0%; Pred. No. 2.5e-56;
iive 31; Mismatches 68
                                                                                                                                                                                                         Disclosure; Page 36-37; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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                                           96WO-US003965
                                                                95US-00409851
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                                                                                     (INDV ) UNIV INDIANA FOUND
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Matches 148; Conservative
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N-PSDB; AAT39546.
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                           Kang C;
                                                                                                                                                                                                                                                                                                                                                      Sequence 255 AA;
                                                                23-MAR-1995;
                                           22-MAR-1996;
WO9629348-A1
                      26-SEP-1996
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                                                                                                          Kwon BS,
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ID AAR7
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AC AAR7
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XX ILA;
KW ILA;
XX ILA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILA may be used to identify a host defence inflammatory response in body tissue. The ILA agents can be used to detect an ILA-mediated pathology such as atherosclerosis, autoimmune disease (rheumatoid arthritis, transplant rejection, pathogenic host defense responses to microorganism and mlignancy such as lung carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 AREPGHSPQIISFFLALISTALLFFLIFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE
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                                                                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                       'note= "casein-kinase-II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                               'note= "protein-kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
                                                                                                                                                                                                                                                                                    'note= "casein-kinase-II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                      /note= "potential N-glycosylation site"
187. .213
/note= "transmembrane domain"
                                                                                               'note= "potential N-glycosylation site"
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57.6%; Pred. No. 3.5e-55;
Mismatches 70;
                                                                                                                                                                                                                                                                                                       241. .244
/note= "potential ligand binding
                           .. .17
'note= "signal peptide"
ocation/Qualifiers
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EDGCSCRFPEEEEGG 252
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N-PSDB; AAR74087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwarz H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                    Misc-difference
                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-1993;
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     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                   Domain
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28

RESULT

Homo sapiens

us-10-067-122b-2.rag

142

202

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This sequence represents a novel human h4-1BBSV receptor protein which is used in a method for making a human 4-1BB receptor splice variant which acts as an antagonist. The antagonist polypeptides may be used to treat/prevent disease states mediated by h4-1BBSV receptors such as endotoxic shock, inflammation, cerebral malaria, activation of the HIV virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding sequences are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
       LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTPEGGPG
                         86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA
                                                                                  ---GHSLOVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding human 4-1BB receptor splicing variant - usin treating h4-1BBSV mediated disease states such as endotoxic shock inflammation, graft rejection and inactivation of HIV.
                                                                                                                                                                                                                                                                                                                                                  h4-1BBSV receptor; human; splice variant; antagonist; treatment; disease prevention; endotoxic shock; inflammation; cerebral malaria; HIV virus activation; graft rejection; bone resorption; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 51.2%; Pred. No. 4.9e-46;
Matches 130; Conservative 27; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .18
/label= signal_peptide
19. .219
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                     AAW92523 standard; protein; 219 AA
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                                                                                                                                                                                                                                                                                                                            Human h4-1BBSV receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gentz
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DGCSCRFPEEEEGG 216
                                                                                                                              DACSCRCPOEEEGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a novel human h4-1BBSV receptor. This is a human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of the tumour necrosis factor (TNF) family of ligands. It is induced by T-cell activation. The h4-1BBSV receptor nucleic acid and protein can be used for diagnosis and therapy. In particular, agonists of h4-1BBSV receptor can be used to treat and/or prevent tumours, restenosis, cytotoxicity, bacterial and viral infection, deleterious effects of ionising radiation, autoimmune disease, AIDS and graft-host rejection, to regulate immune responses, wound healing and cellular proliferation. Antagonists can be used to treat and/or prevent endotoxic shock, inflammation, cerebral malaria, activation of the HIV virus, graft rejection, bone resorption and cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGNSCYNIVATLLLLVLNFERTRSLQDPCSNCP-------32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AGVFRITRKECSSISNAECDCIPGFHCLGAGCSMCEQDCKQGQELTKKGCKDCC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 4-1BB receptor splicing variant and related DNA - used to develop products for treating e.g. tumours, viral infection, endotoxic chock, autoimmune disease or bone resorption.
                                                                                                                                 h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxic shock; tumour necrosis factor; TNF ligand; T-cell activation; inflammation; tumour prevention; viral infection; autoimmune disease; cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                                                                                                                                            /note= "soluble extracellular domain"
151. 177
/note= "transmembrane domain"
                                                                                                                                                                                                                                                       1. .18
/note= "putative signal sequence"
                                                                                                                                                                                                                                                                                                  /note= "mature protein"
                                                                                                                                                                                                                                        Location/Qualifiers
                AAW31759 standard; protein; 219 AA
                                                                                                      A novel human h4-1BBSV receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                         (first entry)
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Matches 130; Conserv
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N-PSDB; AAT88969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ni J, Yu G,
                                                                                                                                                                                                             Homo sapiens
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                                             AAW31759;
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Peptide
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236
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                                                                              121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                     8
 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a human h4-1BBSV receptor protein variant which has antagonistic properties. This protein may be used to treat/prevent disease states mediated by h4-1BBSV receptors such as endotoxic shock, inflammation, cerebral malaria, activation of the HIV virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding sequences are useful in gene therapy. This sequence does not appear in the specification but has been created from the wild-type sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human 4-1BB receptor splicing variant - useful in treating h4-1BBSV mediated disease states such as endotoxic shock, inflammation, graft rejection and inactivation of HIV.
                                                                                                FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA
                                                                                                                                                  -----AGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDCC
                                                                                                                                     ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE
                         CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33. .34 /note= "Site of deletion of residues GTFCDNNRNQICSPC PPNSFSSAGGQRTCDICRQCK corresponding to amino acid residues 34-69 of the wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                 malaria;
                                                                                                                                                                                                                                                                                                                                                                                                h4-1BBSV receptor; human; splice variant; antagonist; treatment; disease prevention; endotoxic shock; inflammation; cerebral malar HIV virus activation; graft rejection; bone resorption; cachexia;
MGNSCYNIVATLLLVLNFERTRSLQDPCSNCP-
                                                                                                                                                                                                                                                                                                                                                                       Human h4-1BBSV receptor protein variant.
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DGCSCRFPEEEEGG 216
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy
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represented in Fig

Sequence 219 AA;

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                                                                                                                                                        121 LGTFNDQNGTGVCRFWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                            ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 236
                                                                                                                                                                                                                           143 REPGHSPQIISFFLALTSTALLFLLFFLTLRFSVVXRGRKKLLYIFKQPFMRPVQTTQEE 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumoun tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock wound healing; autoimmune disease; acquired immunedeficiency syndrome; AIDS; graft-host rejection; cellular proliferation; cerebral malaria; bone resorption; human immunodeficiency virus; HIV; graft rejection; inflammation; antibacterial; immunosuppressive; vulnerary; vasotropic; antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
                                                                                                                               -----AGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDCC
                                                                                                                                                                        86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-APA
                                                    1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTPCRKYNPVCKSCPPSTFSSIGGQPN
                                                                                                     CNICRVCAGYPRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
                          Gaps
                          42;
  Length 219;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19. .219 _ _ ____/label= Mature_human_h4-1BBSV_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human h4-1BB splicing variant (h4-1BBSV) receptor.
                        55,
45.9%; Score 656; DB 2;
51.2%; Pred. No. 4.9e-46;
iive 27; Mismatches 55
                                                                    /label= Extracellular_domain
151. 177
/label= Transmembrane_domain
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/label= Signal_peptide
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97US-00816605.
99US-00253549.
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                                                                                                                                                                                                                                                               DACSCRCPQEEEGG 250
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DGCSCRFPEEEEGG 216
 Query Match 45.9%
Best Local Similarity 51.2%
Matches 130; Conservative
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YU G.
GENTZ R.
DILLON P J.
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13-MAR-1997;
22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001
                                                                                                                               33
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                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                 AAE08545;
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The present invention relates to an isolated human 4-IBB receptor splicing variant (h4-IBBSV, where 4-IBB is a member of tumour necrosis factor (TNF) family of ligands) polypeptide. h4-IBBSV cDNA is used in gene therapy. h4-IBBSV is useful for research, biological, clinical and therapeutic purposes. h4-IBBSV, its fragments, analogues or derivatives are useful as an immunogen to produce antibodies which are useful for isolating and identifying clones expressing the polypeptide or to purify the polypeptide. h4-IBBSV is useful for disorders of cells, tissues and organisms and treatment of disorders of cells, tissues and organisms and its nucleic acid is useful for detecting complementary polynucleotides for e.g. as a diagnostic reagent and for chromosomal identification. h4-IBBSV receptor agonists are useful for preventing, treating tumours, restenosis, cytotoxicity, autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-construction and antagonists are useful for treating and/or preventing endotoxic shock, inflammation, cerebral malaria, activation of human communodeficiency virus (HIV) virus, bone resorption, graft rejection and immunodeficiency virus (HIV) virus, bone resorption, graft rejection and immunodeficiency virus (HIV) virus, bone resorption.
                                                                           New human 4-1BB receptor splicing variant polypeptides and polynucleotides, useful for research, diagnosis, prevention and treatment of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency syndrome and graft rejection.
                                                                                                                                                                                                                       Claim 15; Fig 1; 28pp; English.
WPI; 2001-529104/58.
N-PSDB; AAD15246.
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61 CNICRVCAGYPRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120 121 LGTENDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180 86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142 ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 236 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60 1 MGNSCYNIVATLLLVLNFERTRSLQDPCSNCP---------------45.9%; Score 656; DB 4; Length 219; 51.2%; Pred. No. 4.9e-46; Live 27; Mismatches 55; Indels ' 250 DGCSCRFPEEEEGG 216 Query Match
Best Local Similarity 51.2
Matches 130; Conservative DACSCRCPQEEEGG Sequence 219 AA; 181 237 g g à дg g δ δ 8

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Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive; anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator; vasotropic; gene therapy; chromosome mapping; extracellular domain; endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease; human immunodeficiency virus; HIV; graft-host rejection; bone resorption; cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;
                      ABB84639 standard; protein; 219 AA.
                                                                                                                  (first entry)
                                                                                                                                                                Human h4-1BBSV receptor.
                                                                                                                  05-FEB-2003
                                                                    ABB84639;
ABB84639
ID ABB8
XX
AC ABB8
XX
XX
DY 05-F
XX
XX
KW Huma
KW Anti
KW endc
KW endc
KW huma
KW cach
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9

Gaps

55; Indels 42; Length 219;

45.9%; Score 656; DB 6; 51.2%; Pred. No. 4.9e-46; tive 27; Mismatches 55;

Query Match Best Local Similarity 51.29 Matches 130; Conservative

Sequence 219 AA;

61 CNICRVCAGYFRFKKFCSSTHNAFCECIEGFFCLGPQCTRCFKDCRPGQFLTKQGCKTCS 120

1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN

g

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This invention describes a novel human h4-1BBSV receptor or a sequence that is at least 85% identical to the h4-1BBSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, antiinflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome company and carrent and chromosome company. h4-1BBSV is useful for diagnosing a disease or susceptibility to a disease related to underexpression of h4-1BBSV or for identifying creceptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV), graft-host rejection, bone resorption or cachexia, tumours, autoimmune disease, ionizing radiation, acquired cimmunodeficiency syndrome (AIDS), for providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells and certain haematopoletic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist. This sequence represents the human 4-1BBSV receptor described in the constitution of the invention
AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated h4-1BBSV receptor polypeptide, useful for treating providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis.
                                                                                                                                                                                               /label= soluble_extracellular_domain
/label= soluble_extracellular_domain
/note= "region specifically claimed in claim la"
                                                                                                                                              19. 219
/label= h4-1BBSV_receptor
/note= "region specifically claimed in claim 1b"
                                                                                                                                                                                                                                                       151. 177 /
/label= transmembrane_domain
                                                                                                           1. 18
/label= leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 1A-B; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1996; 96US-0013474P.
13-MAR-1997; 97US-00816605.
22-FEB-1999; 99US-00253549.
19-DEC-2000; 2000US-00739394.
                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2002; 2002US-00097330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-066900/06.
N-PSDB; ABS57520.
                                                                                                                                                                                                                                                                                                             US2002127651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu G,
                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 12-SEP-2002
                                                                                                 Key
Peptide
                                                                                                                                                   Protein
                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                           Domain
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Gaps

42;

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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.

The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists, antagonists and antibodies exhibit cytostatic, dermatological, antianaemic, antiantial anticological antiniar in the treatment of antial arthritis or inflammatory, neuroprotective, noctropic, antiparkinsonian, and cerebroprotective activity. The methods are useful for treating arthritis or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
                                236
                                                                                                                                                                 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency
                                                                                                                           ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor-receptor related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY94714 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 16; 373pp; English.
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99US-0126522P.
99US-0135169P.
99US-0147383P.
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DGCSCRFPEEEEGG 216
                                                                                                                                                                                                                                                            237 DACSCRCPQEEEGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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ROSEN C A.
GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200056405-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY94714;
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(ROSE/)
(GENT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 33
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XXX
AAY
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DE 29-
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dermatitis, allergic encephalomyelitis, rheumation arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency disorders (such as severely combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2, TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, barkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human 4-1BB protein. The sequence was used in the characterisation of the TR2 receptor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDCCFGTFNKQK-RGICRPWTNCSLDGKSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumous necrosis factor, e.g., in treating inflammation or autoimmune diseases.
preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 CDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKFCSSTHNAECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 CIEGFHCLGPQCTRCEXDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host disease; skin allergic reaction; immune complex disease; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                     Match 34.9%; Score 499; DB 3; Length 132; Local Similarity 63.9%; Pred. No. 2.3e-33; es 85; Conservative 13; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF-R extracellular Cys-rich domain 4-IBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW94650 standard; peptide; 69 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00866545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 LKTGTTEKDVVCG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LVNGTKERDVVCG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV PENNSYLVANIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-080781/07.
                                                                                                                                                                                                                                                                                                                                                Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94650
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AAW94650
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Disclosure; Fig 1; 78pp; English.

The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF. They may be used in treating TNF-associated conditions such as acute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral, transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R from the present invention

Sequence 69 AA;

; 0 Query Match 18.8%; Score 268; DB 2; Length 69; Best Local Similarity 63.8%; Pred. No. 1.2e-14; Matches 44; Conservative 8; Mismatches 17; Indels DCRPGOELT 112 104 19 엄 δ 셤

AAB69202 standard; protein; 69 AA. AAB69202;

(first entry)

Human TNF-R extracellular Cys-rich domain 4-IBB SEQ ID NO:11.

Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast; osteoclastoclastoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic; antirheumatic; antiarthritic; antiniflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis; Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation;

Homo sapiens

WO200108699-A1

08-FEB-2001.

28-JUL-2000; 2000WO-US020510

(UYPE-) UNIV PENNSYLVANIA. (AOKI/) AOKI K. (HORN/) HORNE W C. (BARO/) BARON R.

Greene MI, Murali R; Baron R, Aoki K, Horne WC,

WPI; 2001-182866/18.

Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for inhibiting osteoclastogenesis and bone resorption.

Disclosure; Fig 1; 81pp; English

The present invention describes a method for inhibiting

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osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNF)-related activation-induced cytokine (TRANCE)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating disease characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal disease, and modulating dendritic cell maturation, T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-R) superfamily member, which is used in the exemplification of the
                  8X8666666666888
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Sequence 69 AA;

44 CKSCPPSTFSSIGGOPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEK 103 Query Match 18.8%; Score 268; DB 4; Length 69; Best Local Similarity 63.8%; Pred. No. 1.2e-14; Matches 44; Conservative 8; Mismatches 17; Indels 셤

104 DCRPGOELT 112 ||: ||||| DCKQGQELT 69 ò

RESULT 36

AAB36700 standard; protein; 415 AA.

(first entry) 15-MAR-2001 Human tumour necrosis factor receptor LTbR protein SEQ ID NO:6.

Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cancer; cardiovascular disorder; viral infection.

Homo sapiens.

WO200071150-A1.

18-MAY-2000; 2000WO-US013515.

20-MAY-1999; 99US-0135164P.

(HUMA-) HUMAN GENOME SCI INC.

Wei Y, Ruben SM, Gentz RL, Ni

WPI; 2001-041051/05.

Nucleic acid encoding a TRID polypeptide, also referred to as tume necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.

Disclosure, Fig 2, 285pp, English.

The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor

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           controprotective, antiviral, antionflammatory, antionvalue, movinging, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRKAECRCQPGMSCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 --AMILIAILISLVLFLLFTTVL--ACAWMRHPSLCRKLGTLLKR------HPEGEESP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 THNAECECIEGFHC--LGPQCTRCEKD----CRPGQEL-----TKQGCKTCSLGTF- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDQNGTGVCRPWTNCSLDGRSVLKTGTTEXDVVCGPPVVSFSPSTTISVTPEGGPGGHSL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTSSPRARCOPHTRCEIOGLVEAAPGTSYSDTICKNP------PEPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 QVLTLFLALTSALLLALIFITLLFSVLKWIR----KKFPHIFKQPFKKTTGAAQEEDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS
                                                                                                                                                                                                                                                                                                                                                                                                        58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour necrosis factor receptor 2 related protein variant; TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy; TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis; asthma; ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 237; DB 4; Length 415; 27.0%; Pred. No. 3e-11; ive 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse lymphotoxin-beta receptor protein SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP96138 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001; 2001US-00917372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 27.0% les 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 SCRCPQEE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |:::
PCPAPRAD
                                                                                                                                                                                                                                                                                                                                        Sequence 415 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus
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ID ABP9
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AC ABP9
XX
DT 09-N
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DE MOUS
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KW TNF
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OS MUS
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The present invention describes human tumour necrosis factor receptor 2 related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic and immunosuppressive activities, and can be used in gene therapy. The TNFR2PV cDNA or protein sequences can be used for preparing a composition for treating a disease or condition associated with increased TNF signalling e.g., cancer of the prostate, ovary, gallbladder, breast, brain, liver or colon, or inflammatory disorders, such as rheumatoid arthritis, asthma or ulcerative colitis. The present sequence represents a mouse lymphotoxin-beta receptor amino acid sequence, which is given in comparison with human TNFR2PV in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AMLLIAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGTLLKR------HPEGEESP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 QVLTLFLALTSALLLALIFITLLFSVLKWIR-----KKFPHIFKQPFKKTTGAAQEEDAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDQNGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTSSPRARCOPHTRCEIQGLVEAAPGTSYSDTICKNP-------PEPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 THNAECECIEGFHC--LGPQCTRCEXD----CRPGQEL-----TKQGCKTCSLGTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                         New cDNA, useful for preparing a composition for treating a disease condition associated with increased TNF signaling e.g., cancer of th prostate, ovary, gallbladder, breast, brain, liver or colon, or rheumatoid arthritis, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 237; DB 6; Length 415; 27.0%; Pred. No. 3e-11; artive 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine osteoclast differentiation and activation receptor
                                                                                                                                                                                                                                 Disclosure; Fig 2A-C; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 27.09
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCRCPQEE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCPAPRAD 276
WPI; 2003-256445/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9846751-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches 6
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98WO-US007584

15-APR-1998;

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The present sequence represents murine osteoclast differentiation and activation receptor (ODAR). The present invention describes cottoucler (ODAR). The present invention describes osteoprotegarin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein companies are used to produce recombinant OPG binding protein. OPG binding protein camples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding oFG binding protein can be used to detect of sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein or Ab, are used to treat or prevent bone diseases, cof OPG binding protein or Ab, are used to treat or prevent bone diseases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, bone of promote bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEEDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NA--ECECIEGEH----CLGPQCTRCEXDCRPG-----QELTXQG-CKTCSLGTFNDQ- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGTGVCRPWINCSLDGRSVLKIGTIEKDVVCGPPVVSFSPSTIISVTP-EGGPGGHSLQV 186
                                                                                                                                                                                                               Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSSMTLRRPPKEAQAYLPSLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%; Score 215; DB 2; Length 625; 28.6%; Pred. No. 3e-09; ive 27; Mismatches 91; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW69958 standard; protein; 625 AA
                                                                                                                                                                                                                                                                                       Example 12; Fig 10; 47pp; English
                97US-00842842.
97US-00880855.
98US-00052521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSCRCPQEEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSSLSGNKESSG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.6
Matches 72; Conservative
                                                                                                                                                            WPI; 1998-594578/50.
                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                               N-PSDB; AAV70304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 625 AA;
                  16-APR-1997;
23-JUN-1997;
30-MAR-1998;
                                                                                                                                                                                                                                                         diagnosis.
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                                                                                                                           Boyle WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
AAW69958
ID AAW6
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AC AAW6
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DT 08-C
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This represents the murine muRANK (receptor activator of necrosis factor-
kappaB (NF-kB)) polypetide which is a homolog of the human RANK. RANK is
a member of the tumour necrosis factor (TNF) family. A soluble RANK may

CC a member of the tumour necrosis factor (TNF) family. A soluble RANK may

CC expressing membrane-associated RANK with a soluble RANK which binds to

CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used

CC SANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used

CC STANK polypeptide composition may also be used for regulating an immune or

CC STANK polypeptide composition of NF-kB by RANK antagonists may be

CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be

CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be

CC csuseful in ameliorating negative effects of an inflammatory response that

CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,

CC calls that express RANK. RANKL polypeptides can also be used to identify

CC cells that express RANK and thus inhibitors of an inflammatory response, and

also for protecting RANK-expressing cells from the negative effects of

CC chemotherapy or the presence of high levels of TNF-alpha. The products

CC can also be used for detection and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 CDNCOPGTF-CRKYNP----VCKSCPPSTF-SSIGGOPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 NA--ECECIEGFH----CLGPQCTRCEXDCRPG-----QELTKQG-CKTCSLGTFNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 NGIGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells.
                                                    RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.1%; Score 215; DB 2; Best Local Similarity 28.6%; Pred. No. 3e-09; Matches 72; Conservative 27; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Maraskovsky E;
                   Murine NF-kB receptor activator muRANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 14; Page 62-64; 80pp; English.
                                                                                                                                                                                                                                                                                                           96US-0059978P.
97US-00813509.
97US-0064671P.
                                                                                                                                                                                                                                                                    97WO-US023775
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                                                                                                                                                                                                                                                                                                                                                                                                IMMV ) IMMUNEX CORP.
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N-PSDB; AAV41379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DM,
                                                                                                                                                                                    WO9828426-A2
                                                                                                                                                                                                                                                                      22-DEC-1997;
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14-OCT-1997;
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08-OCT-1998

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This represents the murine muRANK (receptor activator of necrosis factor-
kappaB (NF-kB)) polypetide which is a homolog of the human RANK. RANK is
a member of the tumour necrosis factor (TNF) family. Host cells
transformed or transfected with an expression vector comprising the RANK
cransformed or transfected with an expression vector comprising the RANK
cransformed or transfected with an expression vector comprising the RANK
concacting nucleic acid can be used to produce recombinant RANK protein.
The soluble RANK may be used for inhibiting activation of NF-kB, by
contacting a cell expressing membrane-associated RANK with a soluble RANK
which binds to RANK ligand (RANKL). The soluble RANK polypeptide
composition may also be used for regulating an immune or inflammatory
response. Inhibition of NF-kB by RANK antagonists may be useful in
ameliorating negative effects of an inflammatory response that result
from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-
versus-host reactions, or acute inflammatory reactions. They can also be
used in adjunct therapy for disease characterised by neoplastic cells
that express RANK. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galibert LJ, Maraskovsky E;
                                                                                                                                                                                                             Murine NF-kB receptor activator muRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page 62-64; 80pp; English
                                                                                                             AAW68294 standard; protein; 625 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0059978P.
97US-00813509.
97US-0064671P.
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                                                                                                                                                                               (first entry)
CSCRCPOEEEGG 250
                            255 CSSLSGNKESSG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-377655/32.
N-PSDB; AAV41373.
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07-MAR-1997;
14-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                              WO9828424-A2
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 239
                                                                                                                                               AAW68294;
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14;

Gaps

CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107 82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ- 127

8

СP $\dot{\delta}$

8

28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH

15.1%; Score 215; DB 2; Length 625; ilarity 28.6%; Pred. No. 3e-09; Conservative 27; Mismatches 91; Indels

Query Match Best Local Similarity Matches 72; Conserv

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108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                        187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEEDA
                                                                         128 NGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV
                                                                                                                                                                                                          | ||::: :: |:||
218 LLLFISV--VVVAAIIFGVYYRKGGKALTANLWNWV-----
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                                                                                                                                                                                                                                                                                                                                                                                                  RANK; necrosis factor-kappa B; NF-KB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; murine.
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Sequence Sequence Sequence

Sequence

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1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
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Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08236918A

Sequence 6, Application US/08236918A

Patent No. 5674704

APPLICANT: Alderson, Mark R.

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MDDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3

SOFTWARE: Microsoft Word, Version #6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELEFHONE: (206) 597-0430
TELEFHONE: (206) 597-0430
TELEFAN: 256 amino acids
LENGTH: 256 amino acids
                 US-09-215-649A-15
US-09-577-780-15
US-09-577-800-15
US-09-871-856-15
US-09-871-856-15
US-09-877-650-15
US-09-041-886-27
US-09-042-785A-10
US-09-042-785A-10
US-09-114-944D-2
US-09-573-986-10
US-09-573-986-10
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US-09-573-986-10
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TOPOLOGY:
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Sequence 139, App
Sequence 53, Appl
                                                                                     5, 2004, 14:35:32; Search time 36.8219 Seconds (without alignments) 358.923 Million cell updates/sec
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                                                                                                                                                              1 MGNNCYNVVVIVLLLVGCEK........DACSCRCPQEEEGGGGGYEL 256
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-623-545A-3
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US-08-795-447A-52
US-08-795-447A-52
US-08-795-447A-52
US-08-795-446B-52
US-08-795-446B-52
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US-08-705-446B-52
US-08-705-946B-52
US-08-816-605-9
US-08-816-605-9
US-09-007-097-2
US-09-573-986-11
US-09-573-986-11
US-09-573-545A-2
US-09-573-545A-2
US-09-573-545A-2
US-09-573-555-0
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US-09-573-986-6
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Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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                                                                                                                             LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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                                                       CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
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APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor TITLE OF INVENTION: That Binds Thereto
FILE REFERENCE: 2801-B
CURRENT APPLICATION NUMBER: US/09/150,864A
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 08/060,843
PRIOR FILING DATE: 1993-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6.
                                                                                                                                                                                                   GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
US-09-150-864A-6
                                                                                                                                                                                                                                                                           241 CRCPQEEEGGGGGYEL 256
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Sequence 2, Application US/08012269A Patent No. 6362325 GENERAL INFORMATION:

US-08-012-269A-2

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APPLICANT: Merckle GmbH

TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE

TITLE OF INVENTION: UTILIZATION OF PERIPHERAL MONOCYTES

FILE REFERENCE: 30424.1USWO

CURRENT APPLICATION NUMBER: US/09/623,545A

CURRENT FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: EPO 98103859.9

PRIOR FILING DATE: 1999-03-05

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 256;
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; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1989-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/09623545A; Patent No. 6627200; GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-623-545A-3
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US-09-623-545A-3
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                                                                                                                      181 GHSLQVLTLFLALTSALLLALIFILLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS 240
                                                                                                                                                                                                                                                                                      121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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                                       1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
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1 MGNNCYNVVVIVILLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
WANTE WASTER ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52, Application US/08974022; Patent No. 6015938; GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J. APPLICANT: Lacey, David L. APPLICANT: Calzone, Frank J. APPLICANT: Chang, Ming-Shi TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CRCPOEFEGGGGGYEL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CRCPÓBBBGGGGGYBL 256
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REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
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Best Local Similarity 100.0'
Matches 191; Conservative
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                                                                                                                              LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                                                                                                                        GHSLQVLTLFLALTSALLLALIFITLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS 240
                                                                                                                                                                                     121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                                                                    GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS 240
     CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
                                          Gaps
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COUNTRY: USA
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELS, Christopher A
REFERENCE/DOCKET NUMBER: KWOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                  CRCPQEEEGGGGGYEL 256
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PCT-US96-03965-2
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                                                                                                             121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ...
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APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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Matches 191; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-795-445A-52
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61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LGTFNDQNGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.0%; Score 1085; DB 3; Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 191; Conservative 0; Mismatches 0;
                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/08974186

Patent No. 6284740

GENERAL INFORMATION:

APPLICANT: Boyle, Willaim J.

APPLICANT: Lacey, David L.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     STREET: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
Sequence 52, Application US/08795447A sequence 52, Application US/08795447A Patent No. 6284728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 191 amino acids
amino acid
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TOPOLOGY: linear
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US-08-974-186-52
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61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 52:
BEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Jinear
MOLECULE TYPE: protein
TYPE: ALGRESS

MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.0%; Score 1085; DB 3; Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 191; Conservative 0; Mismatches 0;
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APPLICANT: Lace, David

APPLICANT: Calzone, Frank
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT APPLICATION NUMBER: 08/577,788
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
SEQ ID NO 139
LENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 139, Application US/08706945D; Patent No. 6369027; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 191; Conservative
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CRGANISM: Homo sapiens
US-08-706-945D-139
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US-08-706-945D-139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.0%; Score 1085; DB 3; Length 191; Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 191; Conservative 0; Mismatches 0; Indels
                                                                                   STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boyle, Willaim J.
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
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US-08-795-446B-52
; Sequence 52, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                 ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
SOFTWARE: PatentI
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US-08-816-605-9
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121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Goodwin, Caig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation SIREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
ITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378 Rev
CURRENT FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%; Score 1085;
100.0%; Pred. No. 1
tive 0; Mismatche
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; Sequence 53, Application US/08577788C
; Patent No. 6613544
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 191; Conservative
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LENGTH: 19
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120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
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; Patent NO. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
; ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.7%; Score 795; DB 1; Length 255; 58.4%; Pred. No. 9.1e-63; iive 31; Mismatches 67; Indels
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PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECPHONE: (206) 597-0430
TELECPHONE: (206) 533-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 EDACSCRCPQEEEGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                       : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.4%
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-236-918A-8
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MEDIUM TYPE: Floppy
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us-10-06/-122b-2.rai

ANDERS A

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121 CFGTFNDQX-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
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APPLICANT: Kwon, Byoung; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB; FILE REFERENCE: 740.011US1; CURRENT APPLICATION NUMBER: US/09/007,097A; CURRENT FILING DATE: 1998-01-14; NUMBER OF SEQ ID NOS: 10; SOFTWARE: FastSEQ for Windows Version 3.0; SOFTWARE: PastSEQ for Windows 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 Score 795; DB 3; 11 Stricty 58.4%; Pred. No. 9.1e-63; Conservative 31; Mismatches 67;
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REGISTRATION NUMBER: 35,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-007-097-2
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Matches 149; Conserva
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EDGCSCRFPEEEEGG 252
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11
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Best Local Simi
Matches 149;
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US-09-578-764A-2
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US-09-578-764A-2
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TYPE: PRT
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                   G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE 235
                                    121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
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APPLICANT: Alderson, Mark R.
APPLICANT: Alderson, Mark R.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor TITLE OF INVENTION: That Binds Thereto
FILE REFERENCE: 2801-8
CURRENT APPLICATION NUMBER: US/09/150,864A
CURRENT PILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 08/060,843
PRIOR FILING DATE: 1993-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGNSCYNIVATLILIVINFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQR
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Patent No. 6455040;
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5;
FILE REFERENCE: 1488.1280004;
CURRENT APPLICATION NUMBER: US/09/573,986;
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27;
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens (clone: hu4-1BB)
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// Patent No. 6355779
// GENERAL INFORMATION:
                                                                                                              238 EDGCSCRFPEEEEG 252
                                                                                   EDACSCRCPOEEEGG 250
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US-09-150-864A-8
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                                                                                                             61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC
                                                                                    1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                                                                                                                                         120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTPEGGP
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                                            Gaps
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Sequence 2, Application US/09578764A

GENERAL INFORMATION:

HITLE OF INVENTION:

FILE REFERENCE: 740.011US1

CURRENT APPLICATION NUMBER: US/09/578,764A

CURRENT FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2.
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   Length 255
                                          Indels
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Pred. No. 9.1e-63;
; Score 795; DB 4;
; Pred. No. 9.1e-63;
31; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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58.4%; Pred
ntive 31;
58.7%;
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Query Match
Best Local Similarity 58.4<sup>§</sup>
Matches 149; Conservative
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KWO5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TEMMETH: 255 amino acids
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                                                  Sequence 2, Application US/09623545A

Sequence 2, Application US/09623545A

Patent No. 6627200

GENERAL INFORMATION:

APPLICANT: Merckle GmbH

TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE

TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES

TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES

FILE REFERENCE: 30424.1USWO

CURRENT APPLICATION NUMBER: US/09/623,545A

CURRENT APPLICATION NUMBER: BPO 98103859.9

PRIOR PILING DATE: 1999-03-05

PRIOR FILING DATE: 1999-03-05

PRIOR FILING DATE: 1999-03-05

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 255

LENGTH: 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 14850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 EDACSCRCPQEEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 EDGCSCKFPEEEEGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-623-545A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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PCT-US96-03965-8
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: 255 amino acids amino acids

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                                                                                                                                                                                                                                                                                                                                                                                                                   121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
                                                                                                                                                                                                                                                                                   60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                                                                                                                                                                  1 MGNNCYNVVVIVILLIVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                 8; Gaps
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(S-08-816-605-2

(S-08-816-605-2

(S-08-816-605-2

(S-08-816-605-2

(GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Noo-Liang

APPLICANT: Rest Receptor Splicing Variant

(NUMBER OF INVENTION: Human 4-IBB Receptor Splicing Variant

(NUMBER OF SAGUENCES:

ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA
                                                                          Ouery Match 55.7%; Score 795; DB 5; Length 255; Best Local Similarity 58.4%; Pred. No. 9.1e-63; Matches 149; Conservative 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRIES 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEMPER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 EDACSCRCPQEEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 EDGCSCRFPEEEEGG 252
MOLECULE TYPE: protein
                             PCT-US96-03965-8
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us-10-067-122b-2.rai

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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTPEGGPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142
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Sequence 55, Application US/09523323

Sequence 55, Application US/09523323

Sequence 55, Application US/09523323

Sequence 55, Application US/09523323

Sequence 55, Application

Pattern No. G635743

APPLICANT: Buber, Reinhard

APPLICANT: Ruben, Steven M.

APPLICANT: Ulrich, Stephen

APPLICANT: Ulrich, Stephen

TITLE OF INVENTION: Apptesis Inducing Molecule II and Methods of Use

TITLE OF INVENTION: Applicant US/09/523,323

CURRENT APPLICATION NUMBER: 06/148,380

EARLIER PELING DATE: 1999-12-02

EARLIER APPLICATION NUMBER: 60/142,657

EARLIER APPLICATION NUMBER: 60/142,657

EARLIER APPLICATION NUMBER: 60/142,657

EARLIER APPLICATION NUMBER: 60/142,641

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 09/252,656

EARLIER APPLICATION NUMBER: 60/075,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.9%; Score 656; DB 2; Length 219; Best Local Similarity 51.2%; Pred. No. 1.5e-50; Matches 130; Conservative 27; Mismatches 55; Indels 4
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPHONE: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
TYPE: amino acid
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61 CTPGFHCLGAGGSMCEQDCKQGQELTKKGCKDCCFGTFNKQK-RGICRPWTNCSLDGKSV 119
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; Sequence 11, Application US/08866545
; Patent No. 6265535
; Patent No. 6265535
; Patent No. 6265535
; APPLICANT: Greene, Mark I.
APPLICANT: Takasaki, Wataru
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 CIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.8%; Score 497; DB 4; Length 132; 63.9%; Pred. No. 9.6e-37; tive 13; Mismatches 33; Indels
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009113-0004-999

TRISCOMMUNICATION INFORMATION:
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1997-03-21
EARLIER FILING DATE: 1997-03-21
EARLIER FILING DATE: 1997-03-27
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 55
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 LKTGTTEKDVVCG 159
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Best Local Similarity 63.99
Matches 85; Conservative
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US-09-523-323-55
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44 CKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEK 103
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US-09-627-775-11

Sequence 11, Application US/09627775

Patent No. 6682739

GENERAL INFORMATION:
APPLICANT: Greene, Mark
APPLICANT: Antali, Ramachandran
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
CURRENT FILING DATE: 2000-07-28

PRIOR FILING DATE: 1999-07-28

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
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US-09-006-353A-6
; Sequence 6, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: GENTZ, REIBER
; APPLICANT: RUBEN, STEVEN
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.8%; Score 268; DB 3; Best Local Similarity 63.8%; Pred. No. 8.2e-17; Matches 44; Conservative 8; Mismatches 17;
TELEPHONE: 650-493-4935
TELERAX: 650-493-5556
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
ENGTH: 69 amino acids
TYPE: amino acids
TYPE: amino acid
TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DCRPGOELT 112
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US-09-627-775-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DCKQGQELT 69
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185 QVLTLFLALTSALLLALIFITLLFSVLKWIR----KKFPHIFKQPFKKTTGAAQEEDAC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 --AMLLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGTLLKR-----HPEGEESP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 16.6%; Score 237; DB 3; Length 415; Best Local Similarity 27.0%; Pred. No. 3.3e-13; Matches 67; Conservative 33; Mismatches 90; Indels
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US-09-573-986-6
; Sequence 6, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, 'Ying-Fei
; APPLICANT: Wei, 'Ying-Fei
; APPLICANT: Reiner
; APPLICANT: Ruben, Steven
; TILLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; TILLE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT PILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
COUNTRY: NOCAVILLE
STATE: ND
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 36,373
RELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TTYPE: amino acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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FILING DATE:
LENGTH:
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                                                                                                                                                                                                                                                        125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEXDVVCGPPVVSFSPSTTISVTPEGGPGCHSL 184
                                                                                                                                                                                                                                                                                                                                                                                      185 QVLTLFLALTSALLLALIFITLLFSVLKWIR-----KKFPHIFKOPFKKTTGAAQEEDAC 239
                                                                                                                                                                                                                                                                                                                                                                                                            220 --AMILIAILLSLVLFILFTTVL--ACAWMRHPSLCRKIGTLLKR-----HPEGEESP 268
                                                                                                                                                                                179 NTSSPRARCOPHTRCEIQGLVEAAPGTSYSDTICKNP------PEPG----
                                                                                                                                                     28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS
                                                                                                               58;
                                                                         16.6%; Score 237; DB 4; Length 415; larity 27.0%; Pred. No. 3.3e-13; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08996139;
Patent No. 6017729;
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER STADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                 ; ORGANISM: Homo sapiens
US-09-573-986-6
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                                                                                            Similarity
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                                                                    Query Match
Best Local Simi
Matches 67;
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US-08-996-139-15
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                                                                                                                                                                                                                                                                                                                                                                                                  128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA :238
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                                                                                                                                                                                                                                                                                                                                                                                                                          28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                            82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ-
                                                                                                                                                                         Gaps
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Sequence 15, Application US/08995659

Patent No. 6242213

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
                                                                                                                                                                         62;
                                                                                                                             Query Match 15.1%; Score 215; DB 3; Length 625; Best Local Similarity 28.6%; Pred. No. 4.6e-11; Matches 72; Conservative 27; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||:: : |:||
218 LLLFISV--VVVAAIIFGVYYRKGGKALTANLWNWV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: USSN 08/772,330
23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins. Patricia
625 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSSLSGNKESSG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSCRCPQEEEGG 250
                                      TOPOLOGY: linear MOLECULE TYPE: protein US-08-996-139-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                    amino acid
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information for the sequence cut; information for the sequence cut; information for the sequence of the sequ	Query Ma	91 QY 28 CDN 107	127 QY 82	186 QV 217	238 Qy 187 254 Ph. 218	239	DP 255 CSSLSG	RESULT 31 US-09-577-780-15 ; Sequence 15, Appli ; Patent No. 6419929 ; GENERAL INFORMAT ; APPLICANT:	; TITLE OF IN ; NUMBER OF S	CORRESPONDE ADDRES STREET CITY:	STATE: COUNTR ZIP: ZIP: GIATE:	COMPUTER KE COMPUT C	SOFTWA CURRENT APPLIC APPLIC	FILING CLASSI CLASSI PRIOR APPLI	APPLICA APPLIC	AFFLIC FILING FI	
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 625 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein	y Match Local Similarity 28.6%; Pred. No. 4.6e-11; hes 72; Conservative 27; Mismatches 91; Indels 62; Gaps	28 CDNCQPGTF-CRKYNPVCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH	82 NAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-CKTCSLGTFNDQ- 	128 NGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV	187 LTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA ::::: : 218 LLLFISVVVVAAIIFGVYYRKGGKALTANLWNWVNDA	39 CSCRCPQBEEGG	255 CSSLSGNKESSG 266	-649A-15 e 15, Application U No. 6271349 AL INFORMATION: APPLICANT: Anderson Galibert	Maraskovsky, Eugene TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:	: Immune 1 Univer ttle	Y: USA 8101 ADABLE FORM:		DATA: MBER: US/09/215, 7-Dec-1998	CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/996,139</unknown>	ATION NUMB DATE: 07 ATION NUMB	DECEMBER 1 ATION: atricia Ar BER: 34,69 NUMBER: 2	-,
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                              48 CSRCEPCKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                     82 NA--ECECIEGFH----CLGPQCTRCEXDCRPG-----QELTKQG-CKTCSLGTFNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV
                                                                                                                                                                                                                                                                                                                                      28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                         Query Match 15.1%; Score 215; DB 4; Length 625; Best Local Similarity 28.6%; Pred. No. 4.6e-11; Matches 72; Conservative 27; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 32
US-09-577-800-15
; Sequence 15, Application US/09577800
; Patent No. 6479635
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/996,139
FILING DATE: 22 DECEMBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
REFERENCE/DOCKET NUMBER: 2852-A
                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/09/577,800
24-MAY-2000
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 24-MAY-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 CSCRCPQEEEGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98101
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128 NGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNBEDKCLLHKVCDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC----SSSWTLRRPPKEAQAYLPSLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGPNCNICRVCAGYFRFKKFCSSTH
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.1%; Score 215; DB 4; Best Local Similarity 28.6%; Pred. No. 4.6e-11; Matches 72; Conservative 27; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
APPLICATION NUMBER: USSN 60/064,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,496
FILING DATE: 17-Dec-1999
CLASSIFICATION: <Unknown>
                                  USSN 08/772,330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-044
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
US-09-466-496-15
; Sequence 15, Application US/09466496
; Patent No. 6528482
; Patent No. 6528482

CRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 CSSLSGNKESSG 266
                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-577-800-15
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18-10-06/-122D-2.rai

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48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNBEDKCLLHKVCDAGKALVAVDPGNH 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEEDA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 NA--ECECIEGEH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTPNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871,291

FILING DATE: 30-May-2001

CLASSIFICATION: <UNKNOWN>
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Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: ...,
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91.
                                                                                                                                                                                                                                                                                                                                                                                                   ;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
US-09-871-291-15
; Sequence 15, Application US/09871291
; Patent No. 6562948
; GENERAL INFORMATION:
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us-10-067-122b-2.rai

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187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 NGTGVCRPWINCSLDGRSVLKTGTIEKDVVCGPPVVSFSPSTIISVIP-EGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSSWTLRRPPKEAQAYLPSLIV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ||::: :: |:||
218 LLLFISV--VVVAAIIFGVYYRKGGKALTANLWNWV----------NDA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CDNCOPGTF-CRKYNP----VCKSCPPSTF-SSIGGOPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%; Score 215; DB 4; Length 625, 28.6%; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels
AIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139
FILING DATE: «Unknown»
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Parricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
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Patent No. 6649164
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
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Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 CSCRCPQEEEGG 250
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STATE: WA
COUNTRY: USA
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108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 NA--ECECIEGEH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%; Score 215; DB 4; Length 625; 28.6%; Pred. No. 4.6e-11; tive 27; Mismatches 91; Indels
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US-09-041-886-27
Sequence 27, Application US/09041886
Fatent No. 6235872
Fatent No. 6235872
Fatent No. 623672
Fatent No. 6236872
Fatent No. 6236872
Fatent No. 6236872
Fatent No. 6236872
Fatent No. 6236873
Fatent Sabizadeh, Sharroz
FITLE OF INVENTION: Proapoptotic Peptides, Dependence
FITLE OF INVENTION: Polypeptides and Methods of Use
FORRESPONDENCE ADDRESS:
FORRESPONDENCE ADDRESS:
FADDRESSEE: Campbell & Flores LLP
FATENTY: San Diego
FATE: California
FATE: California
FATE: California
FATE: California
FATE: San Diego
FATE: San Diego
FATE: California
FATE: California
FATE: California
FATE: California
FATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                FILING DATE: 050 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-877-650-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 625 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 28.6
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 CSLGTF-NDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 GPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFK-----K 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 NLGLRVQQKGTSETDTICTCBEGWHCTSBACESCVLHRSCSPGFGVKQIATGVSDTICEP
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Sequence 10, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.6%; Score 208.5; DB 3; Length 276; Best Local Similarity 25.7%; Pred. No. 7e-11; Matches 67; Conservative 37; Mismatches 108; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 NTAAPVQETLHGCQPVTQEDG 266
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                                                                  NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              TYPE: amino acids
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-041-886-27
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFOI
NAME: Campbell, (
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70 Y--FREKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG------QELTKQGCKT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDP 85
                                                                                                                                                                                                                                                                                                   Length 277;
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Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
APPLICANT: TO GUO-LIANG
APPLICANT: GENTZ, REINER
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                   108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 CPVGFPSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQ----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.7%; Pred. No. 7e-11;
Matches 67; Conservative 37; Mismatches 1
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ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)22/-/400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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11;
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                                                                                                                                                                                                                                                   26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGSSFFLDTWNRETHCHQHKYCDP 85
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                                                                                                                                                                                                                          18 CEKVGAVQNS--CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGOPNCNICRVCAG
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                                                                                                                                                                                   49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 CPVGFFSNVSSAFEKCHPWISCEIKDLVVQQAGINKIDVVCGPQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08114944D

Patent No. 6376459

Jeneral Information:

APPLICANT: Ledbetter, Jeffrey A

APPLICANT: Stamenkovic, Ivan

APPLICANT: Stamenkovic, Ivan

APPLICANT: No. 637645911e, Randolph

TITLE OF INVENTION: THE CD40CR RECEPTOR AND LIGANDS THEREFOR

FILE REFERENCE: 5624-232-999

CURRENT APPLICATION NUMBER: US/08/114,944D

CURRENT FILING DATE: 1992-02-14

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

LENGTH: 277
                                                                                                                                          14.6%; Score 208.5; DB 3; Length 277; larity 25.7%; Pred. No. 7e-11; Conservative 37; Mismatches 108; Indels 49,
                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 NTAAPVOETLHGCOPVTOEDG 266
277 amino acids
                                 Los: single
linear
                                                         TOPOLOGY: linear MOLECULE TYPE: protein US-09-006-353A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo sapiens US-08-114-944D-2
                                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conserva
                     TYPE: amino acid
STRANDEDNESS: siz
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190 -DRLRALVVIPIIFGILFAILLVLVFIK---KVAKKPTNKAPHPKQEPQEINFPDDLPGS 245

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us-10-06/-122D-2.rapp

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model OM protein - protein search,

5, 2004, 14:40:42 ; Search time 94.6849 Seconds (without alignments) 749.438 Million cell updates/sec May Run on:

US-10-067-122B-2 1428 1 MGNNCYNVVVIVLLLVGCEK......DACSCRCPQEEEGGGGGYEL

Title: Perfect score: Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1138120 Total number of hits satisfying chosen parameters:

1138120 segs, 277189581 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

1: \(\cgn2 = \) \(

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	DB	ID	Description
	1428	100.0	256	13	US-10-027-199-10	Sequence 10, Appl
7	1428	100.0	256	74	US-10-067-122-2	. Sequence 2, Appli
ო	1085	76.0	191	디	US-09-405-032-136	Seguence 136, App
4	795	55.7	255	σ	US-09-739-394-9	Sequence 9, Appli
2	795	55.7	255	σ	US-09-826-212-11	Sequence 11, Appl
9	795	55.7	255	σ	US-09-935-727-13	13,
7	795	55.7	255	10	US-09-877-336-2	Sequence 2, Appli
æ	795	55.7	255	13	US-10-097-330-9	Sequence 9, Appli
σ	795	55.7	255	13	US-10-027-199-2	'n
10	795	55.7	255	14	US-10-170-997-2	ď
11	795	55.7	255	14	US-10-186-643-11	Ξ
12	795	55.7	255	14	US-10-207-655-160	7
13	795	55.7	255	15	US-10-418-242-13	급
14	656	45.9	219	Q	US-09-739-394-2	Sequence 2, Appli
15	656	45.9	219	13	US-10-097-330-2	Sequence 2, Appli

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15 US-10-375-680-55	US-10-087-192-9	US-09-826-212-	372-	US-09-935-727-	US-09-917-372-	US-10-186-643-	US-10-418-242-	9 US-09-871-856-15	US-09-877-650-1	12 US-09-865-363-15	US-10-151-071	12 US-09-957-944-4	US-10-166-232A-	-878	9 US-09-839-339A-1	-008-69	9 US-09-768-779A-2	6	9 US-09-826-212-10		9 US-09-935-727-12	US-10-328-	14 US-10-291-480-4	14 US-10-186-643-10	ш,	9 US-09-855-528-2	09-957-94	9 US-09-915-593-6	14 US-10-283-105-6
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ALIGNMENTS

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                                                                                              TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND TITLE OF INVENTION: METHODS; TITLE OF INVENTION: METHODS; FILE REFERENCE: 740.013US2; CURRENT APPLICATION NUMBER: US/10/027,199; CURRENT FILING DATE: 2001-12-20; PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 08/955,572; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22; PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/461,652; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03; NUMBER OF SEQ ID NOS: 12; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 10; LENGTH: 256
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               Sequence 10, Application US/10027199
Publication No. US20020168719A1
GENERAL INFORMATION:
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US-10-027-199-10
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us-10-067-122b-2.rapb

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COUNTRY: USA
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61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
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                                                            GHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQEEDACS
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                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MURINE 4-1BB GENE
FILE REFERENCE: 740.009US1
CURRENT APPLICATION NUMBER: US/10/067,122
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 08/012,269
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: US 07/922,996
PRIOR FILING DATE: 1992-07-30
PRIOR FILING DATE: 1988-11-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 136, Application US/09405032;
Publication No. US20030207827A1
GENERAL INFORMATION:
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive;
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10067122; Publication No. US20030100745A1; GENERAL INFORMATION:
                                                                                                                                                                241 CRCPQEEEGGGGGYEL 256
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Yu, Guo-Liang
Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 191;
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Belease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/405,032
FILING DATE: 24-Sep-1999
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.0%; Score 1085; DB 11; Best Local Similarity 100.0%; Pred. No. 1.1e-88; Matches 191; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378-CIP2
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-405-032-136
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                   Query Match 55.7%; Score 795; DB 9; Length 255; Best Local Similarity 58.4%; Pred. No. 1e-62; Matches 149; Conservative 31; Mismatches 67; Indels
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US-09-826-212-11
Sequence 11, Application US/09826212
Patent No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 255
APPLICATION NUMBER: 09/253,549
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-394-9
                                                                                                                                                                                     LENGTH: 255 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 EDACSCRCPOEEEGG 250
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Matches 149; Conservative
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ORGANISM: Homo sapiens
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61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC 120
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                                            180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
                                 120 SLGTFNDONGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRFGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.7%; Score 795; DB 9; Length 25 Best Local Similarity 58.4%; Pred. No. 1e-62; Matches 149; Conservative 31; Mismatches 67; Indels
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238 EDGCSCRFPEEEEGG 252
                                                                                                        EDACSCRCPQEEEGG 250
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; ORGANISM: Homo sapiens
US-09-935-727-13
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61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC 120
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; Sequence 2, Application US/10027199
; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHODS
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05
; RIOR APPLICATION NUMBER: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
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                                                                                                                                                                                                                                                                                                                  Length 255;
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Pred. No. 1e-62;
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PRIOR APPLICATION NUMBER: US 09/253,549
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: US 08/816,605
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1996-03-15
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 255
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Best Local Similarity 58.4%
Matches 149; Conservative
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19; Conservative
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US-10-097-330-9
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US-10-027-199-2
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121 CFGTFNDQK-RGICRPWINCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177
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                                          180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPPKKTTGAAQE
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kwon, Byoung
TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON
TITLE OF INVENTION: PROTEIN 4-1BB
FILE REFERENCE: 740.011U33
CURRENT APPLICATION NUMBER: US/09/877,336
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 1998-01-14
PRIOR APPLICATION NUMBER: 09/007,097
PRIOR FILING DATE: 1998-01-14
PRIOR PILING DATE: 1995-03-23
PRIOR FILING DATE: 1995-03-23
PRIOR FILING DATE: 1995-03-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 9, Application US/10097330
Publication No. US20020127651A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT FILE REFERENCE: PF254DIC2
CURRENT APPLICATION NUMBER: US/10/097,330
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/739,394
PRIOR FILING DATE: 2000-12-19
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                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09877336 Publication No. US20030000851A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.4%;
Matches 149; Conservative 31
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US-09-877-336-2
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                                      MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
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US-10-186-643-11
; Sequence 11, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
APPLICANT: Wi, Jian
; APPLICANT: Ruben, Steven
; TILLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; TILLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; TILLE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643
; CURRENT APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
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US-10-207-655-160
; Sequence 160, Application US/10207655
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238 EDGCSCRFPEEEEGG 252
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Best Local Similarity 58.4<sup>†</sup>
Matches 149; Conservative
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CRGANISM: Homo sapiens
US-10-186-643-11
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                                                             120 SLGTFNDONGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                   121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
                                                                                                                                      180 G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE
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US-10-170-997-2
; Sequence 2, Application US/10170997
; Publication No. US20030082157A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: New Receptor and Related Products and TITLE OF INVENTION:

APPLICANT: Application US/1017097

Application No. US20030082157A1

GENERAL INFORMATION: New Receptor and Related Products and TITLE OF INVENTION: New Receptor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170,997
FILING DATE: 12-Jun-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DAIA:
APPLICATION NUMBER: US/08/955,573
APPLICATION NUMBER: US/08/955,573
APPLICATION NUMBER: 08/460,976
FILING DATE: <URNOWN>
APPLICATION NUMBER: US 08/122,796
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 08/267,577
FILING DATE: 07-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KWO4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TELEPHONE: 607-273-1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 255 amino acids TYPE: amino acid
                                                                                                                                                                                                                       236 EDACSCRCPOBEBGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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TOPOLOGY: linear MOLECULE TYPE: protein
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US-09-739-394-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCDICRQCKGVFRIRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELIKKGCKDC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
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PRIOR APPLICATION NUMBER: 60/373,604

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2000-11-21

PRIOR PLING DATE: 2000-08-25

PRIOR PLING DATE: 2000-08-25

PRIOR PLING DATE: 2000-08-25

PRIOR PLING DATE: 2000-08-25

PRIOR PELING DATE: 2000-08-25

PRIOR PLING DATE: 1999-12-01

PRIOR PLING DATE: 1999-12-01

PRIOR PLING DATE: 1999-08-02

PRIOR PLING DATE: 1999-08-02

PRIOR PLING DATE: 1999-04-30

PRIOR PLING DATE: 1999-04-30

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P3
CURRENT APPLICATION NUMBER: US/10/418,242
CURRENT FILING DATE: 2003-04-18
                                        APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 160
                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.7%; Score 795; DB 14; Length 255; Best Local Similarity 58.4%; Pred. No. 1e-62; Matches 149; Conservative 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/10418242
Publication No. US20040013664A1
GENERAL INFORMATION:
Publication No. US20030118592A1 GENERAL INFORMATION:
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US-10-207-655-160
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                                                                                                                                                                                                                                                            60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                            120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
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                                                                                                                                                                                                                              1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09739394

Patent No. US20010014465A1

GENERAL INFORMATION:

// GENERAL INFORMATION:

// Guo-Liang

Gentz, Reiner

// TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant

NUMBER OF SEQUENCES:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD
                                                                                                                                                                                       α
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                                                                                                                                            Length 255;
                                                                                                                  55.7%; Score 795; DB 15; Length 2
58.4%; Pred. No. 1e-62;
Micmatches 67; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/253,549
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEPHONE: 301-309-8504
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COMPUTER READABLE FORM:
                                                                                                                                     Query Match
Best Local Similarity 58.4<sup>1</sup>
Matches 149; Conservative
; SEQ ID NO 13
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-13
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61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180 86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142 181 ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 236 ---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 236 61 CNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEXDVVCGPPVVSFSPSTTISVTPEGGPG 180 86 FGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60 Gaps Gaps 42; 42; Query Match
Best Local Similarity 51.2%; Pred. No. 2.1e-50;
Matches 130; Conservative 27; Mismatches 55; Indels 4 Sequence 2, Application US/10097330

Sequence 2, Application US/10097330

Publication No. US20020127651A1

GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
FILE REFERENCE: PF254D1C2
CURRENT APPLICATION NUMBER: US/10/097,330

CURRENT FILING DATE: 2002-03-15

PRIOR APPLICATION NUMBER: US 09/739,394

PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-03-13

PRIOR FILING DATE: 1999-03-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

LENGTH: 219

LENGTH: 219 Length 219; 55; Indels Query Match 45.9%; Score 656; DB 9; Best Local Similarity 51.2%; Pred. No. 2.1e-50; Matches 130; Conservative 27; Mismatches 55. ; US-09-739-394-2 203 DGCSCRFPEEEEGG 216 237 DACSCRCPOREEGG 250 TYPE: PRT
CORGANISM: Homo sapiens
US-10-097-330-2 RESULT 15 US-10-097-330-2 181 g 상. 원 \$ G 8 ò g 셤 δ d $\overset{\circ}{\circ}$ D 8

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87 CIEGEHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTPGFHCLGAGCSMCEQDCXQGQELTXKGCKDCCFGTFNKQK-RGICRPWTNCSLDGKSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 55, Application US/10375680

| Sequence 55, Application US/10375680
| Publication No. US20040009147Al
| GENERAL INFORMATION:
| APPLICANT: Enher, Reinhard
| APPLICANT: Yu, Guo-Liang
| APPLICANT: Ulrich, Stephen
| APPLICANT: Ulrich, Stephen
| APPLICANT: Ulrich, Stephen
| APPLICANT: Ling Date: 1488.065006
| CURRENT FILING DATE: 2003-02-28
| PRIOR FILING DATE: 2002-03-01
| NUMBER OF SEQ ID NOS: 70
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 CDNCQPGTFCR-KYNPVCKSCPPSTFSSIGGOPNCNICRVCAGYFRFKKFCSSTHNAECE
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US-10-087-192-939
; Sequence 939, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 402
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Pred. No. 8.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%; Score 497; DB 15;
63.9%; Pred. No. 1.7e-36;
tive 13; Mismatches 33;
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Best Local Similarity 63.9%;
Matches 85; Conservative
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CORGANISM: Mus musculus
US-10-087-192-939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-375-680-55
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Best Local Similarity
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237 DACSCRCPOFEEGG

203 DGCSCRFPEEEGG 216

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SENERAL INFORMATION:
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    Gaps 12;
                                                   80 THNAECECIEGFHC--LGPQCTRCEXD----CRPGQEL-----TKQGCKTCSLGTF- 124
                                                                                                                  125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSL 184
                                                                                                                                                                                                                          185 QVLTLFLALTSALLLALIFITLLFSVLKWIR-----KKFPHIFKQPFKKTTGAAQEEDAC 239
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                              28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 --AMLLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGTLLKR------HPEGEESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGO-PNCNICRVCAGYFRFKKF--CSS
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    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 16.6%; Score 237; DB 9; Length 415; l Similarity 27.0%; Pred. No. 8.9e-13; 67; Conservative 33; Mismatches 90; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei

APPLICANT: Ruben, Steven

APPLICANT: Ruben, Steven

APPLICANT: Ni, Jian

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280006

CURRENT APPLICATION NUMBER: US/09/826,212

CURRENT FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

LENGTH: 415
                                                                                                                                                                                         192 NTSSPRARCOPHTRCELOGLVEAAPGTSYSDTICKNP----
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  33; Mismatches
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US-09-907-372-20
; Sequence 20, Application US/09907372
; Patent No. US20020068242A1
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09826212
Patent No. US20010021516A1
Conservative
                                                                                                                                                                                                                                                                                                                        PCPAPRAD 289
                                                                                                                                                                                                                                                                                          240 SCRCPQEE 247
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US-09-826-212-6
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67;
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Best Local S
Matches 67
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Sequence 8, Application US/09935727

Sequence 8, Application US/09935727

Patent No. US20020150583A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REPERENCE: PF454P2

CURRENT APPLICATION NUMBER: US/09/935,727

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/303,224

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 415;
APPLICANT: Lal, Preeti G.
APPLICANT: Warren, Bridget A.
TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT FILE REFERENCE: PC-0050 US
CURRENT APPLICATION NUMBER: US/09/907,372
CURRENT FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 g600223
US-09-907-372-20
                                                                                                                                                                                                                                                                                                                                                                                                                                16.6%; Score 237; DB 9; 1
27.0%; Pred. No. 8.9e-13;
tive 33; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.0%
Matches 67; Conservative
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 SCRCPQEE 247
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Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.6%; Score 237; DB 10; Length 415; Best Local Similarity 27.0%; Pred. No. 8.9e-13; Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                              80 THNAECECIEGFHC--LGPQCTRCEKD----CRPGQEL-----TKOGCKTCSLGTF- 124
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US-09-917-372-20
; Sequence 20, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Lal, Preeti G.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT:
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL PROGRAM
; SEQ ID NO 20
LENGTH: 415
; TYPE: PRT
; ORGANISM: MUS musculus
; SEATONDE.
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; OTHER INFORMATION: Incyte ID No. US20030068619A1 g600223
US-09-917-372-20
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 415
TYPE: PRT
                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-935-727-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 SCRCPQEE 247
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	n 415; Is 58	ZAGYFRE	-TKOGC	, otdvac	risvtpegg 	PFKKTTO	1 1		Alpha and
w	Length Indels	- CRKYNPVCKSCPPSIFSSIGGQ-PNCNICRVCAGYFRFKKF : ::: CSRSODTVCKTCPHNSYNEHWNH.STCOLOREPRY.		VTDEIM	SFSPST	PHIFKOI : :	GTLLKR		φ .
Receptor	DB 14; 8.9e-13; hes 90;	GGQ-PN	-CRPGOEL-	PGTEAE	CKNP	KKF	SLCRKL		Receptors
6 4 6 4 3 K	37; E Jo. 8.9 natches	STESSI	CR	RLVLCQ	TEKDVV : : :SYSDTI	.KWIR	ЗАЙМКНР		
3 / 1 / 1 / 3 / 3 / 3 / 3 / 3 / 3 / 3 /	Score 237; DB Pred. No. 8.9e 3; Mismatches	VCKSCPE	CTRCEKI	CVHCEEE	SVLKTG1 VEAAPG1	rrrsvi :	rviAC		
on US/10186643 330118546A1 1-Fei teiner teven 1.1280004 NUMBER: US/10/ 2002-07-02 MBER: US/09/57: 1.27 mer. 2.1		CRKYNP' :	Odbu	VYLDNE	CSLDGR. : CEIQGL	LALIFI' :	ĹŦĹĹŔŦ		on US/10418242 al. Tumor Necrosis 4R3 NUMBER: US/10/4 2003-04-18 MMBER: 60/373,60 002-04-19 MMBER: 09/935,72
ication US/10 US20030118546 ION: Ying-Fei Jian tz, Reiner tz, Steiner En Steiner ION: Tumor Ne 1488,1280004 IION NUMBER: DATE: 2002-0 ON NUMBER: US ID NOS: 27 tIn Ver: 2.1	vat	F	TEGFHC	, Pemsc	CRPWTN : CQPHTR	LTSALL	ıllısıv	247	ion US/104 0040013664A 0040013664A 1 Tumor Nec 154P3 1 NUMBER: U 2 2003-04 1 UMBER: 60/ 1 UMBER: 60/ 2002-04-19
	/ Match Local Similarity les 67; Conser	CDNCOPGIFCCSRCPPGRFFVFAV	THNAECECIEGFHCLGPQCTRCEKD	RECRO	NDQNGTGVCRPWINGSLDGRSVLKTGTTEKDVVCGPP	ALTLFLA 	-AMÍLLÁILLSLVLFILFTTVÍACAWWRHPSLCRKLGTLLKR	SCRCPQEE :: PCPAPRAD	pplicat NUSCONTION MILLON MILLS EN MILLS EN MILLON
UT 22 0-186-643-6 quence 6, Appliblication No. U NERAL INFORMATI PPLICANT: Wei, PPLICANT: Wei, PPLICANT: Wei, PPLICANT: Wei, PPLICANT: Wei, PPLICANT: APICANT ILE REFERENCE: URRENT APPLICATI U	atch cal Sir 67;	28 29 20—CI	. 0	119 DE	125 N 179 N	185 0	220	240 SC 269 PC	-242-8 e 8, Ap tion No INFORM ANT: GE OF INVE T PILIN APPLICA APPLICA APPLICA
RESULT 22 US-10-186-643 Sequence 6, Publication GENERAL INF APPLICANT: APPLIC	Query Match Best Local Matches 6								RESULT 23 US-10-418-242-8 Sequence 8, A Publication N GENERAL INFOR TITLE OF INV TILLE REFEREN CURRENT FILLI PRIOR APPLIC PRIOR PILING PRIOR PILING
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220 --AMLLLAILLSLVLFLIFTVL--ACAWWRHPSLCRKLGTLLKR------HPEGEESP 268

240 SCRCPQEE 247
| | : : 269 PCPAPRAD 276

us-10-067-122b-2.rapb

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239 CSCRCPQEEEGG 250
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US-09-877-650-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSL 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90; Indels
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
16.6%; Score 237; DB 15;
Best Local Similarity 27.0%; Pred. No. 8.9e-13;
Matches 67; Conservative 33; Mismatches 90;
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APPLICATION NUMBER: US/09/871,856
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-27
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Patent No. US20020081720A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 SCRCPOEE 247
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                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY, AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELECHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 215; DB 9;
Pred. No. 1.3e-10;
27; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 625 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.1%;
Best Local Similarity 28.6%;
Matches 72; Conservative 2
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14;

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108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.1%; Score 215; DB 9; Length 625; Best Local Similarity 28.6%; Pred. No. 1.3e-10; Matches 72; Conservative 27; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||::: :: |:||
| LLLFISV--VVVAAIIFGVYYRKGGKALTANLWNWV---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
DATE: 08-Jun-2001
ICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secuence 15, Application US/09865363
Publication No. US20020086826A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101
COMPUTER READABLE FORM:
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PRIOR APPLICATION: CLASSIFICATION: CLASSIFICATION DATA:

APPLICATION NUMBER: 08/995,659
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)587-0430
TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids

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108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGRGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                      128 NGTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                            187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA
                                                                                                                                                                                                  28 CDNCOPGTF-CRKYNP----VCKSCPPSTF-SSIGGOPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                              48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                     82 NA--ECECIEGEH----CLGPQCTRCEKDCRPG-----QELTKOG-CKTCSLGTFNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-151-071-2
US-10-151-071-2
Sequence 2, Application US/10151071
; Sequence 2, Application US/10151071
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: DOUGALL, William
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 625
                                                                                            15.1%; Score 215; DB 12; 28.6%; Pred. No. 1.3e-10; tive 27; Mismatches 91;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-865-363-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 CSCRCPQEEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 CSSLSGNKESSG 266
                                                                                                     Query Match
Best Local Similarity 28.6
Matches 72; Conservative
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RESULT 29

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127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NDA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTLFLALTSALLLALIF------ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CDNCOPGTF-CRKYNP----VCKSCPPSTF-SSIGGOPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ČSRČEPČKYLSSKCTPTSDSVČLPČGPDEYLDTWNEEDKČLLHKVČDAGKALVAVDPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
; Sequence 2, Application US/10166232A
; Publication No. US20030021785A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William, C.
; TITLE OF INVENTION: USE OF RANK ANTAGONISTS TO TREAT CANCER
; CURRENT APPLICATION NUMBER: US/10/166,232A
; CURRENT FILING DATE: 2002-06-05
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||::: :: |:||
218 LLLFISV---VVVAAIIFGVYYRKGGKALTANLWNWV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.1%; Score 215; DB 14; Best Local Similarity 28.6%; Pred. No. 1.3e-10; Matches 72; Conservative 27; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/405,878
FILING DATE: 01-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
US-10-405-878-15
Sequence 15, Application US/10405878
Publication No. US20030175840A1
GENERAL INFORMATION:
HAPLICANT: Anderson, Dirk M.
Galibert, Laurent
Galibert, Laurent
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RESULT 32
US-10-369-300-4
; Sequence 4, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: IMMUNE
; TITLE OF INVENTION: IMMUNE
; TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                  70 Y-~FRFKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG------QELTKQGCKT 118
                                                                                                                                                                                                                            119 ÇSLGTFNDQNGTG-VÇRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
                                                                                                                                                                                                                                                                                                                      178 GPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFK-----K 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 RC--EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TCLQHTTCPPGGRVEKGTHDQDTVCADCLTGTFSLGGTQEECLPWTNCSAFQQEV-RRG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 TIEKDVVCGPPVVSFSPSTTISVTPEG-GPGGHSLQVLTLFLALTSALLLALIFITLLFS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 TNSTDTTCSSQVVYYVVSILLPLVIVGVGIAG------FLICTRRHLHT-----SS 240
                                                                      26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWDRETHCHQHKYCDP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DNTFRLVPCVFLLNLLQRISAQPSCRQEBFLVGDECCPMCNPGYHVKQVCSEHTGTVCAP 77
                                                                                                                                                                86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEP
                                      18 CEKVGAVQNS--CDNCOPG----TFCRKYNPV-CKSCPPSTF-SSIGGOPNCNICRVCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NNCYNVVVIVLLLVGCEKVGAV------ONSCDNCQPG----TFCRKY-NPVCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 CPPSTFSS-IGGOPNCNICRV---CAGYFRFKKFCSSTHNAECECIEGFHCL---GPQCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 212.5; DB 15; Length 276; 27.5%; Pred. No. 8.4e-11; cive 30; Mismatches 108; Indels 65;
                                                                                                                                                                                                                                                        210 VLKWIRKKFPHIFKOPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 VAKEL-----EPFQ------QEQQENTIRFPVTEVG 265
                                                                                                                                                                                                                                                                                                                                                                                                                  229 TTGAACEEDACSCRCPOEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 NTAAPVQETLHGCQPVTQEDG 266
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US-09-768-779A-2
; Sequence 2, Application US/09768779A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 77; Conserv
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Setent No. US20020031512A1

GENERAL INFORMATION:

APPLICANT: TANOX, INC.

APPLICANT: PASCH, M.

APPLICANT: THOMAS, David

TITLE OF INVENTION: CD40 Antagonists For Use in Treating Psoriasis and Other Inflamma

TITLE OF INVENTION: Skin Conditions

TITLE OF INVENTION: Skin Conditions

TITLE OF INVENTION: Skin Conditions

FULLE REFERENCE: TNX00-05

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: 60/198,174

PRIOR APPLICATION NUMBER: 60/198,174

PRIOR FILING DATE: 2000-04-19

NUMBER: Patentin version 3.0

SEQ ID NO 1

LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNREDKCLLHKVCDAGKALVAVDPGNH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 LTLFLALTSALLLALIF-----ITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 NA--ECECIEGFH----CLGPQCTRCEKDCRPG------QELTKQG-CKTCSLGTFNDQ- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 TAPRRCACTAGYHWNSDC----ECCRRNTECAPGFGAOHPLOLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CDNCQPGTF-CRKYNP----VCKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.1%; Score 215; DB 14; Length 625; Best Local Similarity 28.6%; Pred. No. 1.3e-10; Matches 72; Conservative 27; Mismatches 91; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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FILING DATE: 14 OCTOBER 1997
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUEC CHARACTERISTICS:
TENERAL COCCUPATION:
                                                                                                                                                                                                                                                                                                                LENGTH: 625 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ 1D NO: 15:
US-10-405-878-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 CSCRCPQEEEGG 250
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; ORGANISM: Human CD40
US-09-839-339A-1
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US-09-839-339A-1
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146 CPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQ-
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JAPPLICANT: Wei, Ying-Pei
APPLICANT: Guben, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Rec
FILE REFERENCE: 1488.1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 277
            CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/768,779
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/086,582
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1997-05-29
PRIOR FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09826212
Patent No. US20010021516A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.4
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-826-212-10
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                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: human
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Best Local Simi
Matches 67;
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                                                                                                                                                                                                                              LENGTH: 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QELTKQG-CKTCS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 -----NSTTPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAQHPLQLNKDTVCKPCL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CDNCQPGTFCRK-----YNPVCKSCPPSTF-SSIGGQPNCNICRVC------AGYF
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US-10-291-480-2
; Sequence 2, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n 14.7%; Score 209.5; DB 9; Length 615; Similarity 30.4%; Pred. No. 3.9e-10; S2; Conservative 25; Mismatches 70; Indels 47
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMSTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/768,779A
FILING DATE: 25-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                        AFFLICANT: MAORE, PAUL
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
RECEPTOR-LIKE PROTEIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 RFKKFCSSTHNAECECIEGFH----CLGPQCTRCEKDCRPG-
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: KENLEY K. HOOVER

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PF368PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

FORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-768-779A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 GGHSLOVLTLFLALTSALLLALIF 203
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                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 615 amino acids
                                                                                                                                 NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
Patent No. US20020127637A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
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Best Local Simi
Matches 62;
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                 46 CNKCEPCKYMSSKCTTTSDSVCLPCGPDEYLDSWNBEDKCLLHKVCDTGKALVAVVAG--
                                                                                                                                                                                                             72 RFKKFCSSTHNAECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCS
                                                                                                                                                                                                                                                                104 -----NSTIPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAQHPLQLNKDIVCKPCL
                                                         Gaps
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                                                         47;
    Length 615;
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14.7%; Score 209.5; DB 14; Length 30.4%; Pred. No. 3.9e-10; iive 25; Mismatches 70; Indels
                                                                                                          28 CDNCQPGTFCRK----YNPVCKSCPPSTF-SSIGGOPNCNICRVC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%; Score 208.5; DB 9; ilarity 25.7%; Pred. No. 1.9e-10; Conservative 37; Mismatches 108;
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OS-09-93-727-72.

Sequence 12, Application US/09935727

Parent No. US20020150593A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

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     190 -DRLRALVVIPIIFGILFAILLVLVFIK---KVAKKPTNKAPHPKQEPQEINFPDDLPGS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTSTECLPCGESEFLDTWNRETHCHQHKYCDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 CEKVGAVQNS--CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGOPNCNICRVCAG
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                                                              229 TIGAAQEEDACSCRCPQEEEG 249
                                                                                                                          246 NTAAPVQETLHGCQPVTQEDG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-727-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 67; Conserve
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                                      178 GPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFK------K 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 Y--FRFKKFCSSTHNAECECIEGFHCLGPQCTRC-、EKDCRPG-----QELTKQGCKT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ÇSLGTF-NDQNGTGVCRPWTNÇSLDGRSYLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETETLPCGESEFLDTWNRETHCHQHKYCDP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CEKVGAVQNS--CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGQPNCNICRVCAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: ...

ZIP: 20850

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/768,779A

FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
FILING DATE: CUNknown>
FILING DATE: CUNknown>
FILING DATE: CUNknown>
HILING DATE: CUNknown>
FILING DATE: CUNKNOWN

HILING DATE: (UNKNOWN)

TELECOMMUNICATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PF366FP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8439

""TAGENTALION OF 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NI, JIAN
MOORE, PAUL
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
RECEPTOR-LIKE PROTEIN 8
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ 1D NO: 4:
US-09-768-779A-4
                                                                                                                       229 TIGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                        246 NTAAPVQETLHGCQPVTQEDG 266
                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09768779A Patent No. US20020127637A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Sequence 323, Application US/10328953
; Publication No. US2004007165641
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Wieland, Felix
; APPLICANT: Wieland, Felix
; TILE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT APPLICATION NUMBER: US/10/328,953
; CURRENT APPLICATION NUMBER: US 60/342,570
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 2002-04-12
; PRIOR FILING DATE: 2002-04-12
; PRIOR FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEO IT NOOF 221
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; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TILE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
; PRIOR FILING DATE: 1998-05-28
; PRIOR FILING DATE: 1998-05-28
; PRIOR FILING DATE: 1998-05-28
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 Y--FRFKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG------QELTKQGCKT 118
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SOFTWARE: WordPerfect 8.0 for Windows
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Best Local Similarity 25.7%
Matches 67; Conservative
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; ORGANISM: Homo sapiens
US-10-328-953-323
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Publication No. US20030118546A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
                                                                                                                                                  14.6%; Score 208.5; DB 14; 25.7%; Pred. No. 1.9e-10; ive 37; Mismatches 108;
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US/09/573,986
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 TIGAAQEEDACSCRCPQEEEG 249
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 277
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CRGANISM: Homo sapiens
US-10-186-643-10
                                                                                                                                                                     Similarity
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Best Local Similarity

// TYPE: PRT
// ORGANISM: human
US-10-291-480-4
                                                                                                                                                Query Match
Best Local S
Matches 67
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190 -DRLRALVVIPIIFGILFAILLVLVFIK---KVAKKPTNKAPHPKQEPQEINFPDDLPGS 245

95 AB

Search completed: May 5, 2004, 14:53:53 Job time : 96.6849 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 5, 2004, 14:34:41; Search time 30.6849 Seconds (without alignments) 802.512 Million cell updates/sec Run on:

US-10-067-122B-2 142B 1 MGNNCYNVVVIVLLIVGCEK.....DACSCRCPQEBEGGGGGYEL 256 Title: Perfect score: Sequence:

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	escription	-cell antigen 4-1	lymphocyte activat	-cell activation	OX40 homolog - hum	TC)	necrosis	cell-associated	tumor necrosis fac	ene murine tumour	death receptor-6 -	X40 antigen precu	CD27 antigen precu	D27 antigen precu	ox40 prc	· =			ical		in alpha-	major surface-labe	growth fac	grin beta-5		erve growth facto	in -	beta-2 c	alpha 5	ecrosis f	
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nebatan partan	laminin alpha-1	tenascin-X - bovin	laminin beta-1 cha	subtilisin-like	subtilisin-like	laminin alpha-1	laminin alph	laminin gamma-1	£	hypothetical prote	probable laminin	laminin gamma-1	laminin beta-1	hypothetical	protein T22A3
S18252	MMMSA	T42629	MMHUB1	G02428	JC6148	S14458	518253	MMHUB2	T22759	T23433	T37316	MMMSB2	MMMSB1	T23064	F87908
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126	125.5	125	124.5	124	124	123.5	123.5	122.5	122.5	122.5	122.5	120.5	120.5	120.5	120.5
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ALIGNMENTS

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A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A;Reference number: A60771; MUID:89093941; PMID:2463309
                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:215268; OMIM:109535
A;Marpos-references: GDB:215268; OMIM:109535
A;Marpos-references: GDB:21520q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>F;21-193/Domain: extracellular #status predicted <EXT>F;194-215/Domain: transmembrane #status predicted <TMM>F;216-277/Domain: intracellular #status predicted <CYT>F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 137552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonats Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment of A;Reference number: 137552; MUID:94170844; PMID:7510240.
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Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDP
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A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 Y--FRFKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG---
                                                                                                                                                                        A;Molecule type: protein
A;Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.6%; Score 208.5; DB 2; Best Local Similarity 25.7%; Pred. No. 2.3e-08; Matches 67; Conservative 37; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-277 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 NTAAPVQETLHGCQPVTQEDG 266
                                                                                                                                                A;Accession: A60771
                                                                                                                                                                                                                                                                                          A; Gene: GDB: CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794; PMID:8262389
                                                                                                                                                                                                       IK,
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
C; Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C; Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
E;1-17/Domain: signal sequence #status predicted <NGS
C; Keywords: glycoprotein; phosphortein; receptor ILA #status predicted
E;18-213/Domain: transmembrane #status predicted <NGN) (covalent) #status predicted
E;242/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
E;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                       В.;
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                                                                                                          R; Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk Bur. J. Immunol. 24, 2219-2227, 1994
A; Title: Molecular and biological characterization of human 4-1BB and its ligand. A; Accession: 138426; MUID:94374434; PMID:8088337
A; Status: preliminary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCDICRQCKGVFRIRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQQGELTKKGCKDC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G---GHSLQVLTLFLALTS-ALLIALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAQE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
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                                                                                                     C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C;Accession: 138426; JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 AREPGHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.7%; Score 795; DB 2; Length 255; Best Local Similarity 58.4%; Pred. No. 1.7e-51; Matches 149; Conservative 31; Mismatches 67; Indels
                                                                       lymphocyte activation-induced receptor ILA precursor - human
                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA; Residues: 1-255 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDGCSCRFPEEEEGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDACSCRCPOSEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
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Accession: I38094
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C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: 154182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
C;Accession: 154182
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequent A;Reference number: 154182; MUID:93252381; PMID:8486360
A;Reference number: 154182
A;Accession: 154183
A;Accession: 154183
A;Accession: 12413.3-12513.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNGTGVCRPWINCSLDGRSVLKTGTTEXDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSRCPPGIYVSAKÇSKIRDIVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 THNAECECIEGFHCL--GPQCTRCE--KDCRPGQELT------KQGCKTCSLGTF-ND 126
                                  --PGCHSLOVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 236
THNAECECIEGFHCLGPOCTRCEXDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC 139
                                                                                                                                                28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQPN-CNICRVCAGYFRFKKF--CSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                      208 EVPGGRAVAAI-LGLGLVLGLLGPLAILLALY-LLRRDQRLPPDAHKPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 SSPSARCQPHÍRČENQGLVEAAPGÍAQSDÍTČKNPLEPLPPEMSGIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 435;
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25.7%; Pred. No. 1e-07;
:ive 26; Mismatches 96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 LTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQ 224
                                                                                                             140 SLDGRSVLKTGTTEKDVVC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.74
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                    237 DACSCRCPORER 248
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A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
C;Superfamily: tumor necrosis factor receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG2>
F;78-119/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: nGF receptor repeat homology <NG4>
F;262-279/Domain: intracellular #status predicted <ITNN>
F;280-461/Domain: intracellular #status predicted <ITNT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
A; Residues: 1-461 <SMI>
A; Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
A; Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R; Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A; Title: A second tumor necrosis factor receptor gene product can shed a naturally occur?
A; Reference number: A36475; MUID:91045991; PMID:2172983
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Cross-references: GDB:125914; CMIM:191191;
Map position: 1p36.2-1p36.2;
Introns: 26/3
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13.8%; Score 197; DB 1; larity 26.3%; Pred. No. 2.4e-07	: : : : :::: : :::: : ::::: : ::::: : ::::::
Conservative 33; Mismatches	QY 190 FLALTSALLLALI FITLLFSVLKWĮRKKFPHIFKQP FKKTTGAAQEEDACSCRCPQ 245
QY 25 QNSCDNCQPGTFCRK-YNPVCKSCPPSTFSSI-GGQPNCNIC-RVCAGYFRFKKFC 77	DD 189 KSRMRALLVIPVVMGILITIFGVFLYIKKVVKKPKDNEMLPPAARRQDPQ 238
DD 51 OMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQAC 110	Qy 246 EEE 248
OY 78 SSTHNABCECIEGEHC-LGPQCTRCEKDCRPGQELTKQGCKTCSLGTF- 124	Db 239 EME 241
125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC	RESULT 8 B38634 tumor necrosis factor receptor type 2 precursor - mouse
NVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQH 22	s: Mus musculus (house mouse) 30-Jun-1992 #sequence_revision 30-Jun-1992
227 TQPTPEPSTAPSTSFL	ccession: B38634; A40254; ewis, M.; Tartaglia, L.A. c. Natl. Acad. Sci. U.S.?
211 LKW	A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor re A;Reference number: A38634; MUID:91187885; PMID:1849278 A;Accession: B38634
Db 284 MTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQ 317	ule type: mRNA ues: 1-474 <lew></lew>
RESULT 7 A46476	A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenki Mol Cell Biol 11 3020_3026 1001
associated surface molecule CD40, long splice form - mouses: Mus musculus (house mouse)	A.Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for the A.Reference number: A40254; MUID:91246168; PMID:1645445
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000 C;Accession: A46476; A46515 D:norrec B W. C12th B:3	A;Accession: A40254 A;Molecule type: mRNA
s, n.m.; clain, b.m. nol. 148, 620-626, 1992 : Differential increase of an alternatively	A;Residues: 1-474 <goo> A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R:Kissonerghis: M: Fellowes: R : Peldmann: M : Chernalowsky: V</goo>
ence number: A46476; MUID:92105763; PMID:1370315	WBL Data Library, May 1995 racterization of the promoter region of th
A;Wolecule type: mRNA A;Residues: 1-305 <tor></tor>	A;Reference number: S54816 A;Accession: S54816 A:Status: preliminary
-references: GB:M83312; NID:g1553058 sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)	KIS>
this translation is not annotated in G ldi, J.C.; Torres, R.; Kozak, C.A.; Cha	A; Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044 C; Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
U. Immunol. 143, 3921-3926, 1992 A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene. A;Reference number: A46515; MUID:93094586; PMID:1281194	receptor; transmembrane protein 1 sequence #status predicted <sig> nor necrosis factor receptor type 2 #status predicted <mat.< td=""></mat.<></sig>
sion: A46515 s: preliminary; not compared with co	F receptor repeat homology <ng1></ng1>
ute Lype: incletc acia -res 1289/, LV	NGF receptor repeat homology <ng4></ng4>
imental source: BALB/c, liver sequence extracted from NCBI backbone (NCBIP:120357)	Query Match Best Local Similarity 26.0%; Pred. No. 1.9e-06; Matches 75; Conservative 26; Mismatches 107; Indels 80; Gaps 15;
nt: For an alternative splice form,	25 QNSCDNCQPGTFCRK-YNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKK 7
iamily: CD27 antigen; NGF receptor repe rds: alternative splicing; transmembrar 44/Domain: NGF receptor repeat homology	Db 52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIR 109
Match 13.1%; Score 186.5; Local Similarity 25.1%; pred No. 19-	76 FCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSL 12
61; Conservative 34; Mismat	IIU ACIKQONKVCACEAGKYCALKIHSGSCRQCMRLSK-CGPGFGVASSRAPNGNVLCKACAP 16
QY 28 CDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQP-NCNICRVCAGYFRFKKFCSS 79	CY 122 GTEND-QNGIGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP 175 : :
80 THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGT	176EGGP
DD 98 ESDIVCTCKEGQHCTSKDCEACAQHIPCIPGFGVMEMATETTDIVCHPCPVGFFSNQSSL 157	525
OY 131 -GVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTL 189	QY 208 FSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEGGGGGYE 255

g

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A49053
CD27 antigen precursor - mouse
N;Alternate names: CD27L receptor; T cell activation antigen CD27
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 11-Sep-1998
C;Accession: A49053 #Solten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, I Bur, J. Immunol. 23, 943-950, 1993
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte A;Reference number: A49053; WUID:93209296; PMID:8384562
A;Accession: A49053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GOPNCNICRVC--AGYFRFKKFCSSTHNAECECIEG-----FHCLGPOCTRCEKDCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LLVGCE----KVGAVQNS-----CDNCQPG----TFC-RKYNPVCKSCPPSTFSSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 NYDICKQCIQCNHRSGSELKONCIPIEDIVCQCRPGIQPRQDSSHKLGVDCV----PCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GPGGHSLQVLTLFLAL
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A;Molecule type: mRNA
A;Residues: 1-250 <GRA>
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
                                                                                                               CDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCBLPMIEKTHCTAL
                                                                     CDNCQPGTFCRKYNP-----VCKSCPPSTFSS-IGGQPNCNICR-VCAGYFRFKKFCSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 11.9%; Score 170.5; DB 2; Length 271; 1 Similarity 24.6%; Pred. No. 1.4e-05; 59; Conservative 19; Mismatches 83; Indels 79
                                                                                                                                                                                                                                                                          CRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTIS 172
                                                                                                                                                                                                                                                                                                        81 HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-----
Pred. No. 1.9e-05; i Mismatches 72;
    Best Local Similarity 30.0%; Pr
Matches 48; Conservative 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen precursor - rat
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Best Local S
Matches 59
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2 (INFR2); NGF receptor repeat homold F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor family, belongs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Keywords: Ovary
F,1-21/Domain: signal sequence #status predicted <SIG>
F,1-21/Domain: signal sequence #status predicted <SIG>
F,52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted F,332-350/Domain: transmembrane #status predicted <TMM>
F,410-475/Domain: death domain #status predicted <DED>
F,551-651/Region: conserved cytoplasmic #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP--PVVSFSPSTTISVTP---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 SSTHNAECECIEGFHCL-----GPQCTRCEXDCRPGQELTKQG-----CKTCSLGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EGGP------GGHSLQVLTLFLALTSALLLALIFITLFS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
                                                                                                                       gene murine tumour necrosis factor receptor 2 protein - mouse (fragment) gene murine tumour necrosis factor receptor 2 protein - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003 C;Accession: 148854 R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome 5, 726-727, 1994 A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene. A;Reference number: 148854; MUID:95178848; PMID:7873884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              death receptor-6 - chicken
death receptor-6 - chicken
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C; Accession: JC7705
R; Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A; Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A; Reference number: JC7705; MUID:21308433; PMID:11414698
A; Accession: JC7705
A; Molecule type: mRNA
A; Residues: 1-651 < BRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 ONSCDNCOPGT----FCRK-YNPVCKSCPPSTFSSIGGQ-PNCNIC-RVCAGYFRFKKFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 OMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSK-CGPGFGVASSRAPNGNVLCKACAPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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C;Comment: This receptor, a member of the tumor necrosis factor ritresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Superfamily: tumor necrosis factor receptor type 1: NGF receptor.
      ---SCLQRDAKVPHVPDEKSQDAVGLE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKWIRKKFPHIFKQPFKKTTGAAQBEDACSCRCPQEBBGGGGGYE 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12,7%; Score 182; DB 2; Length 45:
Best Local Similarity 26.6%; Pred. No. 3.1e-06;
Matches 76; Conservative 25; Mismatches 109; Indels
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            NCIILVQRKKKP------
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Query Match

12;

Gaps

79;

79 98 139

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239

171

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gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: 148700; 148334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; E
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interpreterence number: 148700; MUID:94044750; PMID:8228223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL: Z21674; NID: 9312827; PIDN: CAA79772.1; PID: 9312828; Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. 1r. J. Immunol. 25, 926-930, 1995; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40; Reference number: I48334; MUID: 95255413; PMID: 7737295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG 115
                                                                                                                                                                                                                                                                                                                                                                                            80 THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TSALLLALIFITLLFSVLKWIRKKFPHIFKOPFKKTTGAAGEEDAC
                                                                                                                                                                                                                                                                          28 CDNCOPGTF----CRKYNPV--CKSCPPS-TFS-SIGGOPNCNICRVCAGYFRFKKFCSS
                                                                                                                                                                                                                                                                                                                                 40 COMCEPCIFLVKDCDQHRKTAQCDPCIPGVSFSPDHHTRPHCESCRHCNSGLLVRN-CTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPSTT----ISVTPEGGPGGHSLQVLTLFLAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LLIALTLGVTARRINCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLCHPCETGFYNEA
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A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAAS9476.1; PID:g732819
                                              F;212-260/Domain: intracellular #status predicted <INT>
F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                 11.7%; Score 166.5; DB 1; Length 260; 25.0%; Pred. No. 2.7e-05; ive 25; Mismatches 85; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 158; DB 2; Length 272; 23.8%; Pred. No. 0.00012; tive 25; Mismatches 87; Indels
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 TANAECACRNGWQCRDKECTECD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: translated from GB/EMBL/DDBJ:Molecule type: mRNA
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                                                                                                                                                                          l Similarity 25.09
63; Conservative
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Best Local Similarity
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                       F;192-211/Domain:
                                                                                                                                              Query Match
Best Local &
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C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra
F; 1-20/Domain: signal sequence #status predicted <NAT>
F; 21-250/Product: CD27 antigen #status predicted <NAT>
F; 21-182/Domain: extracellular #status predicted <EXT>
F; 21-182/Domain: NGF receptor repeat homology <NG1>
F; 27-63/Domain: NGF receptor repeat homology <NG2>
F; 121-179/Region: proline/serine/threonine-rich
F; 183-202/Domain: transmembrane #status predicted <TMN>
F; 203-250/Domain: intracellular #status predicted <INT>
F; 203-250/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %) Cross-references: GDB:132582; OMIM:186711

%) Cross-references: GDB:132582; OMIM:186711

%) Cross-references: GDB:132582; OMIM:186711

%) Introns: 46/1; 90/1; 150/1; 180/1; 220/1

%; Introns: 46/1; 90/1; 150/1; 180/1; 220/1

%; Superfamily: CD27 antigen; NGF receptor repeat homology

%; Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface antigen; signal sequence #status predicted <NGS-

F; 21-260/Product: CD27 antigen #status predicted <MAT-

F; 21-191/Domain: extracellular #status predicted <EXT-

F; 21-191/Domain: NGF receptor repeat homology <NG3-

F; 55-105/Domain: NGF receptor repeat homology <NG2-
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Reference number: A46454; MUID:92013149; PMID:1655907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ь
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;Title: Genomic organization and chromosomal localization of the human CD27 gene.;Reference number: A46517; MUID:93094588; PMID:1334106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 TANAECSCSKNWQCRDQECTECDPPLNPA--LTRQPSETPSPQP------PPTH- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man)
Date: 18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change 22-Jun-1999
Accession: A46517; A46454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNCOPGTF----CRKYNPV--CKSCPPST-FS-SIGGOPNCNICRVCAGYFRFKKFCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 CRACEPGTFFVKDCEQDRTAAQCDPCIPGTSFSPDYHTRPHCESCRHCNSGFLIRN-CTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 ALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD27 antigen precursor - human
N;Alternate names: CD27L receptor; T cell activation antigen CD27
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lote: sequence extracted from NCBI backbone (NCBIP:120386)
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                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 169.5; DB 1
27.0%; Pred. No. 1.6e-05;
iive 29; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: not compared with conceptual translation
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Best Local Similarity 27.0°
Matches 62; Conservative
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A, Title: Genes of variola and vaccinia viruses necessary to overcome the host protective A, Reference number: S32385, MUID: 93202281; PMID: 8384129
A, Accession: S32385
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A; Residues: 1-3106 <RES>
A; Cross-references: EMBL:U12147; NID:g699109; PIDN:AAC52165.1; PID:g699110
B; Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A; Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2)
A; Reference number: S50829; MUID:95179178; PMID:7874173
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A;Molecule type: mRNA
A;Residues: 64-281 <XUH>
A;Residues: 64-281 <XUH>
A;Cross-references: GB:S75315; NID:g833929; PIDN:AAB33573.1; PID:g833930
B;Chang, A.C.; Wadsworth, S.; Coligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A;Title: Expression of merosin in the thymus and its interaction with thymocytes.
A;Reference number: 148655; MUID:93346725; PMID:8345183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assession: alpha-2 chain precursor - mouse laminin alpha-2 chain precursor - mouse laminin alpha-2 chain precursor - mouse laminin M chain; merosin heavy chain C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text_change 10-Dec-1999 C;Accession: I49077; S50829; I48655; S31576; S53868 R;Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y. Matrix Biol. 14, 447-455, 1995 A;Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mo A;Reference number: I49077; MUID:95316259; PMID:7795883 A;Accession: I49077 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                        C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology F;32-66/Domain: NGF receptor repeat homology <NGF> F;68-109/Domain: NGF receptor repeat homology <NG2> F;110-151/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 9.7%; Score 138; DB 2; Length 34: Local Similarity 22.6%; Pred. No. 0.0042; es 59; Conservative 28; Mismatches 104; Indels
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A;Molecule type: mRNA
A;Residues: 2162-2204,'D',2206-2213,'EY',2216-2279 <RE2>
                                                                                                                                       A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 ----OPFKKTTGAAQEEDACS 240
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Best Local S:
Matches 59
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                                                                                                                                                     hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain India-1967, ssp. major, isolate Ind3
B;Xolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H PA;Reference number: S46868
A;Accession: S46868
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N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 ---ILTSELTITMNHTDCNPVFREEXFSVLNKVATSGFFTGENRYQNISKVCTLNFEIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 138; DB 2; Length 348
22.6%; Pred. No. 0.0042;
cive 28; Mismatches 104; Indels
176 SDAECRDLHPRWTTHTPSLAGSDSPE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----OPFKKTTGAAQEEDACS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.69
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reference number: A36859
Accession: D36858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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C;Function: interact with cells and with other basement membrane proteins to promote C;Superfamily: laminin alpha-1 chain, laminin G repeat homology; laminin-type EGF-like homology; laminin-type EGF-like homology; laminin-type EGF-like homology ciEO15
F;23-3106/Product: laminin alpha-2 chain #status predicted col; extracellular matrix; glycc F;1-22/Domain: signal sequence #status predicted col; extracellular matrix; glycc F;23-3106/Product: laminin-type EGF-like homology ciEO15
F;40-462/Domain: laminin-type EGF-like homology ciEO25
F;410-462/Domain: laminin-type EGF-like homology ciEO35
F;465-511/Domain: laminin-type EGF-like homology ciEO35
F;720-750/Domain: laminin-type EGF-like homology ciEO35
F;710-1033/Domain: laminin-type EGF-like homology ciEO35
F;710-1033/Domain: laminin-type EGF-like homology status atypical ciEO35
F;710-1033/Domain: laminin-type EGF-like homology status atypical ciEO35
F;710-1033/Domain: laminin-type EGF-like homology ciEO35
F;710-1033/Domain: laminin-type EGF-like homology ciEO35
F;710-1033/Domain: laminin-type EGF-like homology ciEO35
F;710-113/Domain: laminin-type EGF-like ciEO35
F;710-113/Domain: laminin-type EGF-like ciEO35
F;710-113/Domain: laminin-type E
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C; Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Sep-1997
C; Accession: A35502
R;Gillin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So, M. Proc. Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990
A; Title: Isolation and expression of the gene for a major surface protein of Giardia lam A; Reference number: A35502; MUID:90280395; PMID:2352929
Cross-references: EMBL:X69869; NID:g53055; PIDN:CAA49502.1; PID:g53056
:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 SIPGSCDSLSGSCLICKPGTTGR----YCELCADGYFGDAVNTKNCQPCR-CDINGSFSE 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       925 DC-HTRTGQCECRPNVQGRHCDECKPETFGLQLGRGCLPCNCNSFGSKSFDCEASGQCWC 983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AVQNSCDN------CQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 FCSSTHNAECEC---IEGFHC------LGPQCTRCEKD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       major surface-labeled trophozoite antigen precursor - Giardia lamblia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1416-1462/Domain: laminin-type EGF-like homology <br/>F;14523-1567/Domain: laminin-type EGF-like homology <br/>F;1523-1567/Domain: laminin-type EGF-like homology <br/>F;2166-2327/Domain: laminin G repeat homology <br/>F;2360-2520/Domain: laminin G repeat homology <br/>F;2546-2709/Domain: laminin G repeat homology <br/>F;2546-233/Domain: laminin G repeat homology <br/>*IG3><br/>F;2960-3106/Domain: laminin G repeat homology <IG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1029 - PPNTTGEKCSECLPNTWGHSI 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16S FSPSTTISVTPEGGPG--GHSL 184
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les 54; Conserva
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A;Molecule type: DNA A;Residues: 1-713 <G1L> A;Cross-references: GB:M33641; NID:g159131; PID:g159132 C;Keywords: surface antigen; transmembrane protein

DB 2; Length 713; 9.5%; Score 135.5;

Query Match

15; 59 PNC-NICRVCAGYF----RFKKFCSSTHNAECE-----CIEGFHCLGPQCTRCEK 103 370 --CIDSCAKIGNYYGATEGAKKLCKECTAANCKTCDDQGQCQACNDGFYKNGDACSPCH- 426 427 -----BSCKTCSAGTASDCTECPTGKALRYGDDGTKGTCGEGCTTGTGAGACK-- 474 15 LVGCE-----KVGAVQNSCD---NCQ-PGTFCR-----KYNPVCKSCPPSTFSSIGGO 82; 475 -TCGLIIDGASYCSECATTTEYPQNGVCAPKASRATPTCNDSPIQNG 520 137 TNCSL--DGRSVLK--TGTTE--KDVVCGPPVVSFSPSTTISVTPEG 177 Pred, No. 0.011; 25.6%; Prec. 58; Conservative Best Local Similarity Matches 58; Conserv g ò d 8 ag ò Š

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nerve growth factor receptor precursor, low affinity - rat N;Alternate names: NGF receptor C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                       integrin beta-5 chain precursor - human
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C; Species: Papio sp. (baboon)
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C; Accession: JC2005
C; Accession: JC2005
R; Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
R; Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
R; Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
R; Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
R; Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.
A; Title: Human and baboon integrin beta 5 subunit-encoding mRNAs have alternative polyad
A; Reference number: JC2005; MUID: 94040831; PMID: 8224922
A; Molecule type: mRNA
A; Residues: 1-656 <SHO>
A; Note: the authors translated the codon AGA for residue 454 as Lys, CAA for residue 471
C; Comment: This protein is a predominant subunit for the vitronectin receptor in baboon C; Superfamily: integrin beta chain; laminin-type EGF-like homology <LEG>
C; Superfamily: call adhesion
F; 320-370/Domain: laminin-type EGF-like homology <LEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 S-IGGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCE--KDCRPGQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 DVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRCAYGYY-QDETTGRCEACRVCEAGSG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 LVFSCQDKONTVCEECPDGTYSDEANHVDPCLPCTVCE-DTERQLRECTRWADAECEEIP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRWITRSTPPEGSDSTAPSTQ---EPEAPPEQDLIASTVAGVVTTVMGSSQPVVTRGTTD 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GPPVVSFS--PSTTISVTPEGGPG-------GHSLQVLT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 TISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI--RKKF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: || |: :: || |:::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-::| |-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;187-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 135; DB 2; Length 656; ilarity 27.7%; Pred. No. 0.012; Conservative 30; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 135; DB 1;
25.2%; Pred. No. 0.0083;
tive 26; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LFLALTSALLLALI 202
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Best Local Similarity 25.2
Matches 65; Conservative
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A;Molecule type: mRNA
A;Residues: 1-799 <MCL>
A;Cross-references: GB:J05633; NID:g186504; PIDN:AAA59183.1; PID:g186505
A;Note: parts of this sequence, including the amino end of the mature protein, were confi
R;Suzuki, S.; Huang, Z.S.; Tanihara, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5354-5358, 1990
A;Title: Cloning of an integrin beta subunit exhibiting high homology with integrin beta-
A;Reference number: A35775; MUID:90319111; PMID:2371275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-192,'A',194-644,'L',646-789,793-799 <SUZ>
A;Residues: 1-192,'A',194-644,'L',646-789,793-799 <SUZ>
A;Cross-references: GB:M35011; NID:g184524; PIDN:AAA52707.1; PID:g306894
R;Ramaswamy, H.; Hemler, M.E.
EMBO J. 9, 1561-1568, 1990
A;Title: Cloning, primary structure and properties of a novel human integrin beta subunit
A;Reference number: S12534; MUID:90228356; PMID:2328726
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C; Species: Homo sapiens (man)
C; Date: 14-Jun-1991 #sequence revision 14-Jun-1991 #text_change 20-Aug-1999
C; Accession: A38308; A35775; S12534; S11708
R; McLean, J.W.; Vestal, D.J.; Cheresh, D.A.; Bodary, S.C.
J. Biol. Chem. 265, 17126-17131, 1990
A; Title: CDNA sequence of the human integrin beta-5 subunit.
A; Reference number: A38308; MUID:91009141; PMID:2211615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GTFNDONGTGVCR----PWTNCSL--DGRSVLKTGTTEKDVVCGPPVV---SFSPST
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A;Residues: 1-644,'L',646-799 <RAM>
A;Cross-references: EMBL:X53002; NID:g33952; PIDN:CAA37188,1; PID:g33953
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C; Superfamily: integrin beta chain; laminin-type EGF-like homology
C; Keywords: cell adhesion; cytoskeleton; duplication; extracellular r
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-799/Product: integrin beta-5 chain #status experimental <MAT>
F;25-719/Domain: extracellular #status predicted <EXT>
F;463-513/Domain: laminin-type EGF-like homology <LEG>
F;720-742/Domain: transmembrane #status predicted <IVM>
F;743-799/Domain: intracellular #status predicted <IVM>
F;743-799/Domain: intracellular #status gredicted <IVT>
F;347,460,477,505,552,586,654,705/Binding site: carbohydrate (Asn) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GDB:128005; OMIM:147561
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Matches 64; Conserv
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pre

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C;Accession: A55677
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal local A;Reference number: A55677; MUID:95213013; PMID:7698745
A;Accession: A55677
A;Status: preliminary; not compared with conceptual translation
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F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F;283-344/Domain: laminin-type EGF-like homology <LE01>
F;347-407/Domain: laminin-type EGF-like homology <LE04>
F;410-467/Domain: laminin-type EGF-like homology <LE04>
F;522-552/Domain: laminin-type EGF-like homology <LE06>
F;83-828/Domain: laminin-type EGF-like homology <LE06>
F;83-824/Domain: laminin-type EGF-like homology <LE07>
F;83-924/Domain: laminin-type EGF-like homology <LE08>
F;877-924/Domain: laminin-type EGF-like homology <LE08>
F;877-934/Domain: laminin-type EGF-
                                         C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             805 KPGVVGRRCDTCAPGYY--GFGPTGCQACQCSPRGALSSLCERTSGQCLCRTGAFGLRCD 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 ACQRGQWGFFSCRPC-VCNGH---ADEC-NTHTGACLGCRDLTGGEHCERCIAGFHGDPR 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 -----ECIEGENCOLICRYCAGYFRFKKFCSSTHNAEC-------ECIEGFH---- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 CDNCQPGTFCRKY-----NPVCKSCPPSTF-SSIGGQPNCNICR-VCAGYFRFKKFCSST 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCDKT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 KVGAVQNSCDNCQPGTFCRKYNPV-CKSC---PPSTFSSI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GDB:132363; OMIM:150325
Map position: 3p21.3-3p21.2
Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                       DB 1; Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AGYGVSGHT--RIG----DVLCTKCPRYTYSDAVSSTET 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:1037-1091/Domain: laminin-type EGF-like homology <LE11>F:1094-1139/Domain: laminin-type EGF-like homology <LE12>F:1142-1186/Domain: laminin-type EGF-like homology <LE13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 ---SLDGRSVLKTGTTEKDVVCGP-PVVSFSPSTTISVT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;985-1034/Domain: laminin-type EGF-like homology <LE10>
                                                                                                                                                                                                                                                                              / Match 9.1%; Score 130.5; DB Local Similarity 25.8%; Pred. No. 0.014; nes 41; Conservative 22; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin beta-2 chain precursor (version 1) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 9.0%; Score 129; DB 2 Local Similarity 25.0%; Pred. No. 0.071; nes 47; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-1797 <WEW>
Cross-references: GB:X79683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 -CLGPQC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
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Best Local S
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MJD:87115859; PMID:3027580
A;Reference number: A26431
A;Residues: 1-425 cRAD>
A;Residues: 1-425 cRAD>
A;Residues: 1-425 cRAD>
A;Residues: 1-425 cRAD>
A;Cession: A26431
A;Residues: 1-425 cRAD>
A;Cession: PH1229; MJD:956755; PIDN:CAA28783.1; PID:956756
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoid A;Reference number: PH1229; MJD:93077038; PMID:1446821
A;Accession: PH1229; MJD:93077038; PMID:1446821
A;Accession: PH1229; MJD:93077038; PMID:1446821
A;Accession: PH1229; MJD:93077038; PMID:1446821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:X61269
Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma o
Comment: The cysteine-rich region of the extracellular domain may form part or all of Comment: The protein is thought to form a high-affinity receptor when it associates we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: myxomma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 15-Sep-2003
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: TNP-alpha receptor-II; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: nerve growth factor receptor; NGF receptor repeat homology; Superfamily: nerve growth factor receptor; Monomer; phosphoprotein; receptor; 1-29/Domain: signal sequence #status predicted <SIG>30-425/Product: nerve growth factor receptor #status predicted <MAT>30-251/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.3%; Score 133; DB 1; Length 425;
Best Local Similarity 25.6%; Pred. No. 0.012;
Matches 51; Conservative 20; Mismatches 88; Indels 40; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 S-IGGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGF-----HCLGPQCTRCEK-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 DVVSATEPČKPČTEČLGLQSMSAPČVEADDAVČRČAYĞYYQDEETGHĆ--EAČSVČEVGS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ----DCRPGQELTKQGCKTCSLGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 LLLLLILGVSSGGAKETCSTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDNVTFS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VIVLLLVGCEKVGAVQ-----NSCDNCQPGTF----CRKYNPVCKSCPPS-TFS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <NEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 EEIPGRWIPRST---PPEG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-20 <MET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Introns: 20/3
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49; Indels 47;

46; Indels 82; Gaps

11;

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---NAECECIEGFHCLGPQCTR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LVSDČPSPGQ-ETVČEVČDKGTPTASQNHVRQCLSČKTČRKEMF-----QVEISPČKADM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 DTVCGCKKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKEKQNTVCNCHAGFFLSGNECTF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 CEKDCRPGGELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP 160
                                    F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                        14 LLVGCEKVGAVQNSCDNCQPGTFCRKYNPV----CKSCPPSTFSSIGGQPNCNICR---
                                                                                                                                                                                            Score 127; DB 1; Length 461;
Pred. No. 0.034;
1; Mismatches 78; Indels 96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $18252; MUID: 92078153; PMID: 1744087
                                                                                                                                                                        66 --VC-AGYFRFKKFCSSTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heparan sulfate proteoglycan - mouse N;Alternate names: perlecan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 IFKQ--PFKKTTG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ICRDSAPVKEVEG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 C-SHCKKNOECMK----
                                                                                                                                                                                                                                                                            58; Conservative
                                                                                                                                                                                                                                    Similarity
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Best Local
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A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptody; Reference number: A36555; MUID:91090841; PMID:1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (cachectin) and
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A; Residues: 1-461 <HIM>
A; Residues: 1-461 <HIM>
A; Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin
C; Superfamily: tumor necrosis factor receptor; transmembrane protein
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
F; 1-29/Domain: signal sequence #status predicted <EXT>
F; 30-211/Domain: extracellular #status predicted <EXT>
F; 30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F; 44-82/Domain: NGF receptor repeat homology <NG1>
F; 44-82/Domain: NGF receptor repeat homology <NG2>
F; 127-167/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                       larvoss
laminin alpha 5 chain - mouse (fragment)
C;Botecies: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Reference number: Z16923
A;Accession: T10053
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3635 <MIN>
A;Residues: 1-3635 <MIN>
A;Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232
C;Genetics:
A;Genetics:
A;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1916 HTTGPHCERCAPGFYGNALLPGNCTRC--DCSPCGTETCDPQSGRCLCKAGVTGQRCDRC 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 STHNAECE-CIEGFH---CLGPQCTRCEKDCRP-------------GQELTK- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 -----QCKTCSLG-----TFNDQNGTGVCRPWINCSLDGRSVLKT----GTT 152
918 LPYGAQCRPCPCPEGPGSQRHFATSCHQDEYSQQIVCHCRAG--YTGLRCEACAPGQFGD 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 SCDNCQPGTFCRKYNPVC--KSCPPSTFSSIGGQPN----CN-ICRVCAGYFRFKKFCS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2030 EKGCRRCQCPRGHCDPHTGHCTCPPGLSGERCDTCSQQHQVPVPGKPGGHGI 2081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 129; DB 2; Length 3635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%; Score 27.2%; Pred. No. 0.12; 27.2%; Pred. No. 0.12; 27.2%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.12;
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                                                                                                                                                           976 PSRPGACQ 983
                                                                               127 QNGTGVCR 134
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Best Local S:
Matches 63
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; References: L-3707 < NOO>
A; Cross-references: EMBL: M77174; NID: 9200295; PIDN: AAA39911.1; PID: 9200296
A; Cross-references: EMBL: M77174; NID: 9200295; PIDN: AAA39911.1; PID: 9200296
A; Cross-references: EMBL: M77174; NID: 980
A; Title: Identification of cDNA clones encoding different domains of the basement membrar A; Reference number: A92680; MUID: 89034110; PMID: 2972708
A; Accession: A31917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 940-1601 < NO2>
A; Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A; Accession: B31917
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 180-2600 < NO3>
A; Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
A; Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
B; Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A; Title: Structural properties of recombinant domain III-3 of perlecan containing a globu
A; Reference number: S66460; MUID:95377282; PMID:7649154
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Has.
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly
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A,Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C,Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Keywords: glycoprotein
;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>;764-811/Domain: laminin-type EGF-like homology <LEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -like homology <LEG>
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A, Residues: 630-642, 'D', 644; 2690-2704 <FUJ>
R; Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.

Eur. J. Biochem. 177, 35-45, 1988
A; Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter
A, Reference number: S01790; MUID:89030693; PMID:3181157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Accession: A31711
A/Accession: A31714
A/Accession: A31714
A/Accession: A31771
A/Accession: A31771
A/Accession: A31771
A/Accession: A31771
A/Accession: A30449
A/Accession: A30499
A/Accession: A30499
A/Accession: A30499
A/Accession: A30499
A/Accession: Biochem. 173, 629-635, 1988
A/Accession: Biochem. 173, 629-635, 1988
A/Accession: S00624
A/Accession: S00624
A/Accession: S00624
A/Accession: A304649
A/Accession: A304649
A/Accession: A30464
A/Accession: A30464
A/Accession: A30464
A/Accession: A30460
A/Accession: A3060
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A/Accession
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Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 19-Jan-2001

Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670

Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.

Biol. Chem. 263, 16536-16544, 1988

Title: Laminin, a multidomain protein. The A chain has a unique globular domain and horpernee number: A31771; MUID:89034134; PMID:3182802
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 153-169 < MAN>

A; Residues: 153-169 < MAN>

R; Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.

Biochem. J. 252, 453-461, 1988

A; Title: Structure and distribution of N-linked oligosaccharide chains on various domain

A; Reference number: S02678; MUID: 88326259; PMID: 2458101

A; Accession: S02678

A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1535 GYVGLSCQDCAPGYTRTGSGLYLGQCELCECNGHSDLCHPETGACSRCQHNTAGEFCELC 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  595 ATGYYGDATAGTPEDCQPCACPLINPENMFSRTCESLGAGGYRCTACE----PG--YTGQ 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VQIHPSR--SV 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 A-GYFRFKKFCSSTHNAECEC-----IEGFHCLGPQCTRCEKDCRPGQELTKQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GCKTCSLGTFNDQN-GTGVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GAVQNSCDNCQPG---TFCRKYNPVCKSCPPSTFSSI-----GGQPNC-----NICRVC 67
                                                                                                                                                                                                                                                                                                                                                                               8.8%; Score 126; DB 2; Length 3707; ilarity 28.1%; Pred. No. 0.21; Conservative 14; Mismatches 66; Indels 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1649 YCEQCAPGYEGDPNVQGGRCQPLTKESLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin alpha-1 chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1687 VPQGGP--HSLR 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 TPEGGPGGHSLQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Appearantly: laminin alpha-1 clain; laminin drepped homology, laminin-type pgF-like homology, laminin alpha-1 clain; laminin drepped homology; laminin-type pgF-like homology solied coil; extracellular pri-24/Domain: signal sequence #status practiced csdcc cMAT>
F;25-3084/Product: laminin alpha-1 chain #status predicted cMAT>
F;25-3084/Product: laminin alpha-1 chain #status predicted cMAT>
F;25-3084/Product: laminin-type EGF-like homology cLEG1>
F;27-371/Domain: laminin-type EGF-like homology cLEG2>
F;277-331/Domain: laminin-type EGF-like homology cLEG2>
F;277-331/Domain: laminin-type EGF-like homology cLEG2>
F;378-519/Domain: laminin-type EGF-like homology cLEG2>
F;376-15/Domain: laminin-type EGF-like homology cLEG3>
F;388-1002/Domain: laminin-type EGF-like homology delatus atypical cLEG5>
F;105-1048/Domain: laminin-type EGF-like homology delatus atypical cLEG5>
F;105-1054/Domain: laminin-type EGF-like homology delatus atypical cLEG5>
F;105-1054/Domain: laminin-type EGF-like homology delatus atypical cLEG5>
F;118-1154/Domain: laminin-type EGF-like homology delatus atypical cLEG5>
F;118-1156/Domain: laminin-type EGF-like homology cLE
A; Accession: S01790
A; Residues: 2538-3084 < DEU>
A; Accession: A30451
A; Accession: A30451
A; Residues: 1911-1929; 1997-2006; 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105; 2120
A; Residues: 1911-1929; 1997-2006; 2033-2045, 'X', 2593-2594; 2600-2610; 2616-2645; 2648-2655; 293; 2998-3005, 'A', 3007-3033, 'V', 3035; 3068-3083 < DE2>
A; Residues: 2256-Val was also found
R; Obsen, D; Nagayoshi, T; Fazio, M; Peltonen, J; Jaakkola, S; Sanborn, D; Sasaki, Jlab: Invest. 60, 772-782, 1989
A; Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, Bl and B2 chan A; Reference number: A34961; MUID: 89280632; FMID: 2733383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-26
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083 <
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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(Gln) (in mature form) #status predicted F.45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718, e (Asn) (covalent) #status predicted F.304-312/Disulfide bonds: #status experimental F.770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experim F.845,2102/Binding site: carbohydrate (Asn) (covalent) #status experimental F.845,2102/Binding site: carbohydrate (Asn) (covalent) #status experimental F.845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description: interact with cells and with other basement membrane proteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1516-2133/Region: handle repeats
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: heptad repeats
F;2150-2308/Domain: laminin G repeat homology <LG1>F;2337-2492/Domain: laminin G repeat homology <LG2>F;2518-2683/Domain: laminin G repeat homology <LG3>F;2518-2683/Domain: laminin G repeat homology <LG3>F;2518-2683/Domain: laminin G repeat homology <LG4>F;2925-3082/Domain: laminin G repeat homology <LG4>F;2925-3082/Domain: laminin G repeat homology <LG4>F;2925-3082/Domain: laminin G repeat homology <LG5>F;2925-3082/Domain: laminin G repeat homology <LG5>F;2
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C;Accession: S13547; A28483; A26994; S23566
R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 15611-15616, 1990
A;Title: Structure of the human laminin B1 chain gene.
A;Reference number: S13547; MUID: 90368768; PMID: 1975589
A;Status: nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1786 (-VUO)
A;Cross-references: GB:M61951; GB:J02778; NID: 9186911; PIDN: AAA59486.1; PID: 9186913
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
B;Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Saras
J. Biol. Chem. 262, 10454-10462, 1987
A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q2;
A;Reference number: A28483; MUID: 87280097; PMID: 3611077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: GDB:119357; OMIM:150240
A;Map position: 7g31.1-7g31.3
A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 523
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description: interact with cells and with other basement membrane proteins to promote of Superfamily: laminin beta-1 chain; laminin-type EGF-like homology (Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular; 1-21/Domain: signal sequence #status predicted <SIG> (22-1786/Product: laminin beta-1 chain #status predicted <MAT> (MAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology #status atypical <LE05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1028-1081/Domain: laminin-type EGF-like homology <1511>:1084-1129/Domain: laminin-type EGF-like homology <1512>-1176/Domain: laminin-type EGF-like homology <1513>-1176/Domain: laminin-type EGF-like Homology <1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology <LE01>
homology <LE03>
homology <LE03>
homology <LE04>
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;549-774/Domain: IV <DOM4>
;773-818/Domain: laminin-type EGF-like homology <LE06>
;773-818/Domain: laminin-type EGF-like homology <LE07>
;821-864/Domain: laminin-type EGF-like homology <LE07>
;867-914/Domain: laminin-type EGF-like homology <LE08>
;917-973/Domain: laminin-type EGF-like homology <LE08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1271-548/Domain: V <DOM5>

1271-332/Domain: laminin-type EGF-like | 1335-395/Domain: laminin-type EGF-like | 1398-455/Domain: laminin-type EGF-like | 1458-507/Domain: laminin-type EGF-like | 1463-468/Region: cell adhesion #status | 1510-540/Domain: laminin-type EGF-like | 1510-540/D
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F;1398-1430/Domain: alpha <ALP>
F;1431-1786/Domain: I <DOM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: mRNA was also sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 762-1786 <VU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S23566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
Gene: GDB:LAMB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: TN-X
C,Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: extracellular matrix; glycoprotein; heptad repeat
                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVCAGYFRFKKFCSS------THNAECE-CIEGFH---CLGPQCTRCE----- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        918 SGVCHLETGLCDCKP--HVTGQQCDQCLSGYYGLDTGLG-CVP-CNCSVEG-SVSDNCTE 972
                                                                                                                                                                                                                                                                                                                     CHLTDGEEVVCDQCAPGYSGSWCERCADGYYGNPTVPGGTCVPC-----NCSGNVD 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDCGQEEPPASACPGGCGPRELCSA---GQCVCVEGFR--GPDCAIQTCPGDCR-GRGEC 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TGVCRPWTNC--SLDGRSVLKTGTTEK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGSCVCODGYAGEDCGEEVPAIEGMRMHLLEETTVRTEWTRAPGNVDAYEIQFIPTTEG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:Y11915; NID:g2462978; PIDN:CAA72671.1; PID:g2462979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: flexilin

[Alternate names: flexilin
[Alternate names: flexilin
[Alternate names: flexilin
[Bocies: Bos primigenius taurus (cattle)
[Accession: T42629
[Accession: T426
                                                                                                                                                                                                                                        CEKVGAVQNSCDNCQP---GTFCRKY-----NPVCK--SCPPSTFSSIGGQPNC--NIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTT
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------CAGYFRFKKFCSSTHNAECECIEGFHCLGPQCT--RCEKDCRPGQELT
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N;Alternate names: laminin chain B1
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           624 CHRRGRCENGRCVCDSGYTGPSC----ATRTCP----ADCRGRGRCVQGVCVCHVGYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ASPPFTARVPSSASAYDQRGLAPGQEYQVTVRALRGTNWGPPASKTITTMIDGPQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVL-------TLFLALTSALLL
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                                                                                                                                       65;
                        Length 3084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.8%; Score 125; DB 2; Length 4135; Best Local Similarity 21.9%; Pred. No. 0.27; Matches 56; Conservative 29; Mismatches 95; Indels 7
                                                                                                                                       Indels
                                                                                                                         58;
              DB 1;
8.8%; Score 125.5; I
26.8%; Pred. No. 0.2;
Live 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 KQGCKTCSLGTFNDQNG-----
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 EKDVVCGPPV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGQCHCGPGV 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-4135 <ELE>
                                                              Similarity
                                                                   Best Local Sim
Matches 51;
                                                                                                                                                                                                                                                                                                                                                       813
                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             973
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RESULT

g à

ò a à g 8 D₂ ò a

g ò 8 F;1431-1786/Region: heptad repeats F;30-35/Disulfide bonds: #status predicted F;120,356,519,677,965,1041,1195,1279,1336,1343,1487,1542,1643/Binding site: carbohydrate F;1179,1182,1785/Disulfide bonds: interchain #status predicted 13; 862 47 96 PPSTFSSIGGOPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFH-----CLG----P 807 APGTFGF--GPSGCKPCB-CHLQGSVNAFCNPV-TGQCHCFQGVXARQCDRCLPGHWGFP 1 MGNNCYNVVVIVLLLV-----GCEKVGAVQNSCD-----NCQPGTFCRKYNPVCKSC Gaps 916 97 QCTRCE-----KDCRP--GOELTKQ-----GCKTCSLGTFNDQ-NGTG-VCRP 135 863 SCQPCQCNGHADDCDPVTGECLNCQDYTMGHNCERCLAGYYGDPIIGSGDHCRP 47; DB 1; Length 1786; Indels 63; ch 8.7%; Score 124.5; DE Similarity 25.9%; Pred. No. 0.15; 45; Conservative 19; Mismatches Query Match Best Local Similarity Matches 45; Conserv 48 g δ В g à

Subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment) C; Species: Homo sapiens (man) C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000 C; Accession: G02428 R; Redelhuber, T.L. submitted to the EMBL Data Library, February 1996 A; Reference number: H01242 A; Reference number: H01242 A; Accession: G02428 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Reference number: H01242 A; Molecule type: mRNA A; Reference number: H01242 A; Accession: G02428 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Molecu

A;Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058 C;Genetics:

A;Gene: PC5 C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C;Keywords: hydrolase; serine proteinase F;148-386/Domain: subtilisin homology <SBT> 61; Indels 104; 8.7%; Score 124; DB 2; Length 899; 22.2%; Pred. No. 0.096; Live 21; Mismatches 61; Indels 10 Local Similarity 22.2 Best Loc Matches

BCIEGFHCLGPQCT-RCE-----KDCRPGQELT------KQGCKTCSLGTF----- 124 629 VGCDGPGPDHCNDCLHYYYKLKNNTRICVSSCPPGHYHADKKRCRKCAPNCESC----FG 684 741 ECRDGLSLQGSRCSVSCEDGRYFNGQDCQPCHRFCATCAGAGADGCINCTEGYFMEDGRC 800 ----NDQNGTGVCRP------WTNC-SLDGRSVLKTGTTEKDVVC 158 85 801 VOSCSISYYFDHSSENGYKSCKKCDISCLTCNGPGFKNCTSCPSGYLLDLGMCQMGAIC 859 VGCEKVGAVQ-NSC------DNCQPGTF-----CRKYNPVCKSCPPSTFS -----PNC----NICRVCAGYFREKKFCSSTHNAEC 54 SIGGQ----685 98 g 8 g $\overset{\diamond}{\circ}$ ΩD $\stackrel{>}{\circ}$ 8

RESULT 35
JC6148
subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human
N;Alternate names: PC6A protease
C;Species: Homo sapiens (man)
C;Daccies: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C;Accession: JC6148
R;Miranda, L.; Wolf, J.; Pichuantes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A;Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1

A, Reference number: JC6148; MUID:96353880; PMID:8755538

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-915 <MIR>
A;Residues: 1-915 <MIR>
A;Cross-references: GB:U56387; NID:g1498312; PIDN:AAC50643.1; PID:g1498313
C;Comment: This protein functions as a soluble enzyme within the secretory pathway. It
C;Genetics:
A;Gene: pc6A
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;164-402/Domain: subtilisin homology <SBT>

. 7

BCIEGFHCLGPQCT-RCE-----KDCRPGQELT------KQGCKTCSLGTF---- 124 757 ECRDGLSLQGSRCSVSCEDGRYFNGQDCQPCHRFCATCAGAGADGCINCTEGYFMEDGRC 816 125 ------NDONGTGVCRP------WINC-SLDGRSVLKTGTTEKDVVC 158 817 VOSCSISYYFDHSSENGYKSCKKCDISCLTCNGPGFKNCTSCPSGYLLDLGMCQMGAIC 875 16 VGCEKVGAVQ-NSC------DNCQPGTF-----CRKYNPVCKSCPPSTFS 54 SIGGQ-------PNC------PNC-----NICRVCAGYFRFKKFCSSTHNAEC 8.7%; Score 124; DB 2; Length 915; 22.2%; Pred. No. 0.097; tive 21; Mismatches 61; Indels 104; Query Match
Best Local Similarity 22.2%
Matches 53; Conservative 98 g ð g ò 셤

laminin alpha-1 chain precursor - human (Species: Homo sapiens (man) (C, Species: Homo sapiens (man) (C, Species: Homo sapiens (man) (C, Species: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 19-Jan-2001 (C, Accession: S14458; S14663; A34961 (C, Accession: S14458; S14663; A34961 (C, Accession: L, I51-160, 1991 (C, A, Title: Molecular cloning of the cDNA encoding human laminin A chain. A, Reference number: S14458; MUID: 91333420; PMID: 1714537 (A, Accession: S14458)

Justice of Compared with conceptual translation
Justice of Status: not compared with conceptual translation
Justice of Status: 1-3075 (HAA>
Justice of Status: 1-3075 (HAA>
Justice of Status: 1-3075 (HAA>
Justice of Status: 1991
Justice of Status: 1991
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Accession: S14663

A; Molecule type: mRNA A; Rolecule type: mRNA A; Residues: 1-227, 'FE', 230-251, 'MLP', 255-418,'E', 420-518,'L',520-1022,'V',1024-1074,'V', J A; Residues: 1-227, 'FE', 230-251, 'MLP', 255-418,'E', 420-518,'L',520-1022,'V', 1024-1074,'V', J A; Cross-references: EMBL:X58531; NID:934225; PIDN:CAA41418.1; PID:934226 R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, J Lab. Invest. 60, 772-782, 1989 A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chas A;Reference number: A34961; MUID:89280632; PMID:2733383

Accession: A34961

A;Status: not compared with conceptual translation A;Molecule type: MRNA A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS> A;Note: the authors translated the codon AGA for residue 2692 as Pro C;Genetics: A;Gene: GDB:LAMA1; LAMA

A; Cross-references: GDE: 120135; OMIM:150320
A; Cross-references: GDE: 120135; OMIM:150320
C; Map position: 18p11.32-18p11.22
C; Map position: 18p11.32-18p11.22
C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Superfamily: laminin alpha-1 chain; calcium binding; cell binding; coiled coil; disulfide bonc F; 1-17/Domain: signal sequence #status predicted <SIG>F; 18-3075/Product: laminin alpha-1 chain #status predicted <MAT>

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tle: Drosophila laminin A chain sequence, interspecies. comparison, and domain structi
ference number: S18253; MUID:92078147; PMID:1744083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNCQPGTF---CRKYNP---
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Best Local Similarity 21.6%
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               A; Gene: FlyBase: LanA
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 10-Dec-1999
C;Accession: S28399; S18253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A;Reference number: S28399; MUID:93049203; PMID:1425586
A;Accession: S28399
A;Actus: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3712 <KUS>
A;Cross-references: GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
B;Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;2142-2300/Domain: laminin G repeat homology <LG1>
F;2142-2300/Domain: laminin G repeat homology <LG2>
F;2329-2484/Domain: laminin G repeat homology <LG2>
F;2510-2676/Domain: laminin G repeat homology <LG3>
F;2534-2536/Region: cell attachment (R-G-D) motif
F;2739-2888/Domain: laminin G repeat homology <LG4>
F;2316-3073/Domain: laminin G repeat homology <LG5>
F;2916-3073/Domain: laminin G repeat homology <LG5>
F;38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,:rate (Asn) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---K 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCKP--NVTGQQCDQCLHGYYGLDSGHG-CRP-CNCSVAG-SVSDGCTDEGQCHCVPGV 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998-1041/Domain: laminin-type EGF-like homology <LEI3>
1044-1087/Domain: laminin-type EGF-like homology <LEI3>
11044-1087/Domain: laminin-type EGF-like homology <LEI3>
11090-1109/Domain: laminin-type EGF-like homology #status atypical <LEI4>
1111-1147/Domain: laminin-type EGF-like homology #status atypical <LEI5>
11160-1159/Domain: laminin-type EGF-like homology #status atypical <LEI6>
11160-1361/Domain: IVa <D04A>
11362-1553/Domain: laminin-type EGF-like homology <LEI8>
11403-1449/Domain: laminin-type EGF-like homology <LEI9>
11509-1553/Domain: cell adhesion #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             871 LKCLG-------NTDGAHCERCADGFYGDAVTAKNCRACECHVKGSHSAVCHLETGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 CDNCQP---GIFCRKY-----NPVC--KSCPPSIFS------SIGGOPNCNIC
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                                                                                                                         homology <LE1>
homology <LE2>
homology <LE3>
homology <LE4>
homology <LE4>
homology <LE4>
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F;18-269/Domain: VI <DOM6>
F;270-516/Domain: V <DOM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;327-394/Domain: laminin-type EGF-like homology <LE3>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;503-512/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology <LE4>
F;709-739/Domain: laminin-type EGF-like homology <LE7>
F;709-739/Domain: laminin-type EGF-like homology <LE3>
F;791-846/Domain: laminin-type EGF-like homology <LE3>
F;902-948/Domain: laminin-type EGF-like homology <LE1>
F;951-995/Domain: laminin-type EGF-like homology <LE1>
F;951-995/Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 RVCAGYFRFKKFCSSTHNAECE-CIEGFH---CLGPQCTRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
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28.5%; Pred. No. 0.28;
Live 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 28.5
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G < DOMG>
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A;Cross-references: FlyBase:FBgn0002526
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like homology <LEG>
C;Reywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular n
F;333-400/Domain: laminin-type EGF-like homology <LEG>
F;333-400/Domain: laminin-type EGF-like homology <LEG>
F;333-400/Domain: laminin-type EGF-like homology <LEG>
F;1776-2115/Domain: laminin-type EGF-like homology <LEG>
F;1809-1856/Domain: laminin-type EGF-like homology <LEG>
F;1809-1856/Domain: laminin-type EGF-like homology <LEG>
F;1809-1876/Domain: laminin-type EGF-like homology <LEG>
F;2017-2061/Domain: repeat G <ARG2>
F;2017-2061/Domain: repeat G <ARG2>
F;2017-2061/Domain: repeat G <ARG2>
F;2064-3048/Domain: repeat G <ARG2>
F;2064-3048/Domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;3334-3528/Domain: repeat G4 <RG4>
F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laminin gamma-1 chain precursor - human
N;Alternate names: laminin chain B2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #text change 10-Dec-1999
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 10-Dec-1999
C;Accession: 31548; A28158; S13549; B34961; S14664; S23567
C;Accession: 266, 221-228, 1991
A;Title: Structure of the human laminin B2 chain gene reveals extensive divergence from A;Reference number: S13548; MUID:91093128; PMID:1985895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 CONCOHNTVGINCNKCKPKYYRPKGKHWNETDVCSPCOCDYFFSTGHCEEETGNCECRAA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RPGQELTKQG----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               545 NQGTESEICHKQSGQCICREGFGGPRCDQCLPGFYNYPD----CKP-CNCSSTGSSAITC 599
A,Molecule type: mRNA
A,Residues: 1762-3712 <GAR>
A,Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VCKSCPPSTFSSIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 FQPPSCDSCAYGYYGYPNCRECECNLNGTNGYHCEAESGQQCPCKINFAGAYCXQCAEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRF-----KKFCSSTHN----ABCECIEGFHCLGPQCTRCEK------DC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 125; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S13548
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.6%; Score 123.5; DB 2;
21.6%; Pred. No. 0.32;
ative 15; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;3079-3200/Domain: laminin G repeat homology <LG3>;3334-3528/Domain: repeat G4 <RG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A;Residues: 1-1609 <KAL>
A;Cross-references: GB:M55217; NID:9186937
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F;1031,1034,1600/Disulfide bonds: interchain #status predicted 80 THNAEC-ECIEG-----2697 NATNRNEÉEN 2706 KTTGAAQEED 237 175 122 228 18 124 40 RESULT T23433 임 δ 엄 δ a δ g g δ δ g ò dd g δ 8 ద ð 73, 1225/1
Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin C; formplex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin C; formplex: Laminins beta-1 chain; laminin-type EGF-like homology
C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C; Superfamily: laminin gamma-1 chain #status predicted <81G>
F; 34-285/Domain: signal sequence #status predicted <81G>
F; 34-285/Domain: laminin-type EGF-like homology <1E01>
F; 34-285/Domain: laminin-type EGF-like homology <1E02>
F; 38-395/Domain: laminin-type EGF-like homology <1E02>
F; 38-395/Domain: laminin-type EGF-like homology <1E04>
F; 48-492/Domain: laminin-type EGF-like homology <1E04>
F; 48-505/Domain: laminin-type EGF-like homology <1E05>
F; 48-505/Domain: laminin-type EGF-like homology <1E07>
F; 560-212/Domain: laminin-type EGF-like homology <1E07>
F; 773-825/Domain: laminin-type EGF-like homology <1E08>
F; 690-1034/Domain: laminin-type EGF-like homology <1E10>
F; 773-825/Domain: laminin-type EGF-like homology <1E10>
F; 773-825/Do RyPickersner, T. Kallunki, T. Tryggvason, K.

J. Biol. Chem. 263, 6751-6756, 1988
J. Prikkearann, T. Kallunki, T. Tryggvason, K.
J. Biol. Chem. 263, 6751-6756, 1988
J. Reference number: Azallash MulD:88198245; PMID:3360804
A. Recession: AZB18
A. Residues: 1-211. 7. 1213-1609 ePIX.
A. Residues: 1-211. 7. 1214-141. 1214.
A. Residues: 1-211. 7. 1214.
A. Residues: 1-211. A;Gene: GDB:LAMC1; LAMB2 A;Cross-references: GDB:120136; OMIM:150290 A;Map position: 1q31-1q31 A;Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1; /3; 1525/1

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2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2518 FFGGPCIQCPRGLTTTSQASTSINSCDTINCIDAN-TMINKNVTVGPSTPYSEICIACEQ 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFNDQNGTGVCRPWTNCSLDGRSVLKT-GTTEKDVV-----CGPPVVSFSPSTTISVT 174
                                                                                  805
                                                                                                                              94 ------GP----QCTRC-----EKDCRP--GQ-----ELTKQGCKTCSLGT 123
                                                                                                                                                                                                864 CKDGFFGNPLAPNPADKCKACNCNPYGTMKQQSSCNPVTGQCECLPHVTGQDCGACDPGF 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGGPGGHSLQVLTLFLALTSALLLALIFITLLF---SVLKWIRK----KFPHIFKQPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PHCLGPQCTRCEKDCRPGQELT-KQGCKTCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GAVQNS-C-DNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKFCSS
                                                                       -----AEC-ECI---EGFHC--
                                                      CEKVG-----AVQNSCDNCQP-----GTFC----RKYNPVCKSCPPSTFSSIGGQPNCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 2824;
DB 1; Length 1609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
8.6%; Score 122.5; DB 2; Length
Best Local Similarity 23.6%; Pred. No. 0.31;
Matches 59; Conservative 31; Mismatches 113; Indels
                            Indels
                                                                                                                                                                                                                                FNDONGTGVCRPWTNC----SLDGRSVLKTGTTBKDVVCGPPV 162
                                                                                                                                                                                                                                                 924 YNLQSGQGCER--CDCHALGSTNGQCDIRTGQCE----CQPGI
                            26;
                                                                                                                63 ICRVCAGYF------RFKKFCSSTHN----
Query Match 8.6%; Score 122.5; I Best Local Similarity 24.2%; Pred. No. 0.2; Matches 54; Conservative 22; Mismatches
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C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3;
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Experimental source: Close EMBL: Close Library, March 1996

A) Reference number: Z19740

A) Accession: T23433

A) Status: preliminary; translated from GB/EMBL/DDBJ

A) Molecule type: DNA

A) Residues: 1-3672 <WIL>
A) Cross-references: EMBL: Z70286; PIDN: CAA94293.1; GSPDB: GN00022; CESP: K08C7.3

A) Experimental source: clone K08C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 GOPNCN--ICRVCAGYFR----FKKFCSSTHNAECECIE------GFHCL----G 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LLLVGCEKVGAVQNSCDNCQPGTF------CRKYNPV--CKSCPPSTFSSIG 56
hypothetical protein KOBC7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T23433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.6%; Score 122.5; DB 2; Length 3672;

Best Local Similarity 28.5%; Pred. No. 0.38;

Matches 49; Conservative 11; Mismatches 49; Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2016 DSCDRCKPDHWGFSRC-----QGCQGCHCGTAAFNTQCNVENGQCTCRP 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 PQCTRCEKD-----CRPGQELTKQGCKTCSLGT--FNDQ-----NGTGVCRP 135
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Search completed: May 5, 2004, 14:41:21 Job time : 32.6849 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 5, 2004, 14:30:56 ; Search time 20.1644 Seconds (without alignments) 661.065 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-067-122B-2 1428 1 MGNNCYNVVVIVLLLVGCEK.....DACSCRCPQEEEGGGGGYEL 256

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	D20334	7	P50284	035305	P25942	959460	035714	P43489	P36941	Q9 y 5u5	P20333	006000	P27512	095407	P25119	075509	008727	008712	Q92956	P15725	Gaebne Gaebne	P41272	Q28203	P26842	P47741	015230	P25943	P18519	P34015	060675	P21849	P24043	P08136	
QI	TOTAL MOTION					TR11_HUMAN	TR18 MOUSE	TNR4 HUMAN	TNR3 HUMAN	TR18 HUMAN	TR1B HUMAN	T11B_HUMAN	TNR5 MOUSE	TR6B_HUMAN	TR1B_MOUSE	TR21 HUMAN	T11B RAT		TR14 HUMAN	TNR4 RAT	TR21 MOUSE	TNR7 MOUSE	TNR5_BOVIN	TNR7 HUMAN	TNR4 MOUSE	LMAS HUMAN	VT2 SFVKA	TR16 CHICK	CRMB_VARV	LMA2 MOUSE	TSA4 GIALA	LMA2_HUMAN	TR16_HUMAN	
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Q07441 papio cynoc Q9ubn6 homo sapien	P18084 homo sapien	073559 cowpox viru	077736 sus scrora	P07174 rattus norv	Q8uya7 camelpox vi	Q9z0w1 mus musculu	P29825 myxoma viru	Q9er63 mus musculu	Q60846 mus musculu	Q61001 mus musculu	
ITBS_PAPCY	TTB5 HUMAN	CRMB_COWPX	TNR6_PIG	TR16 RAT	CRMB CAMPS	TR16 MOUSE	VT2 MYXVL	TR23 MOUSE	TNR8 MOUSE	LMAS_MOUSE	
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ALIGNMENTS

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Schwarz H.;
Submitted (MAR-1999)
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Submitted (OCT-1999)
                           FROM N.A.
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TISSUE=Blood;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNICRVCAGYFREKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen).
TNFRSF9 OR ILA OR CD137.
Homo sapiens (Human).
                                                                                                                                                                                                                                  CYTOLINITAL.
CYTOLLASHIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1428; DB 1; Length 256; 100.0%; Pred. No. 2e-110; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                         FACTOR RECEPTOR
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                                                                                                                                                                                        SUPERFAMILY MEMBER 9.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                          TUMOR NECROSIS
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               PDB; 1D0J; 26-SEP-01.
MGD; MGI:1101059; Tnfrsf9.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 1.
SWART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 1.
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Conservative 0;
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les 256; Conser
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., McMin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Funcan and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16903(2002).
                                         Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.; "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watts T.H.;
"CD28-independent, TRAF2-dependent costimulation of resting T cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwarz H., Tuckwell J., Lotz M.;
"A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor
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MEDLINE=98078711; Pubmed=9418902;
Arch R.H., Thompson C.B.;
"4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of human homologue of 4-1BB and its ligand."; Immunol. Lett. 45:67-73(1995).
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MEDLINE=98270914; PubMed=9607925;
Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.
Kwon B.S.;
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                                                                                                                                                                                                                                    Eur. J. Immunol. 24:2219-2227(1994)
MEDLINE=94374434; PubMed=8088337;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94085794; PubMed=8262389;
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MGNNCYNVVVIVLLVGCEKVGAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP

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G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQE

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                                                                                            MEDLINE=21662677; PubMed=11804328;

MEDLINE=21662677; PubMed=11804328;

A Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;

A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-mediated signal transduction.";

Mol. Cells 12:304-312(2001)

C -! FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.

C -: SUBMIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with LRR-repeat protein 1/LRR-1.

C -: SUBMIT: SECRIFICITY: Expressed on the surface of activated T cells.

C -: SIMILARITY: Contains 4 TNFR-Cys repeats.

C -: DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
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R EMBL; L12944; AAA62478.2; -..

R EMBL; BC006196; AAH06196.1; -..

R EMBL; BC006196; AAH06196.1; -..

R EMBL; BC006196; AAH06196.1; -..

R Genew; HGNC:11924; TNFRSF9.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0006917; P:receptor activity; TAS.

R GO; GO:0006917; P:induction of apoptosis; TAS.

R GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

R GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

R GO; GO:0008285; P:negative regulation of cell proliferation; R Pfam; PF00020; TNFR_C6.

R PARAT; SM00208; TNFR_C6.

R PROSITE; PS00062; TNFR_NGFR_1; 1.

R PROSITE; PS00062; TNFR_NGFR_2; 1.
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EXTRACLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.

INTERACTS WITH LRR-1.

BY SIMILARITY.

BY SIMILARIT
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4-1BB ligand.";
J. Exp. Med. 187:1849-1862(1998)
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STRAIN=CVB; TISSUE=Lung;
MEDLINE=96072804; PubMed=7594541;
Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
Browning J.L., Ware C.F.;
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding, and expression.";
J. Immunol. 155:5280-5288(1995).
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MEDLINE=96278943; PubMed=8663299;
Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
Yagita H., Okumura K.;
"TRAFS, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor.";
J. Biol. Chem. 271:14661-14664(1996).
-!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 and TRAFS. May play a role in the development of lymphoid organs
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-!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
Associates with TRAF3 and TRAF4 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Honjo T.;.
"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 3 precursor (Lymphotoxin-beta receptor).
LTBR OR TNFRSF3 OR TNFCR.
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SEQUENCE FROM N.A.
MEDLINE=96163885; PubMed=8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
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238 EDGCSCRPPEEEEGG 252
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(Receptor activator of NF-KB) (Osteoclast differentiation factor
                                                               TNFRSF11A OR RANK.
Mus musculus (Mouse)
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    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTSSPRARCQPHTRĆEIQGLVEAAPGTSYSDTICKNP-----PÉPG---- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 QVLTLFLALTSALLLALIFITLLFSVLKWIR-----KKRPHIFKQPFKKTTGAAQEEDAC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Gaps
                                                                                                                                                                                                                                              MGD; MGI:104875; Ltbr.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TR11 MOUSE STANDARD; FAL, VOLUME OSS305; Q8VCT7; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) Tumor necrosis factor receptor superfamily member 11A precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%; Score 237; DB 1; Length 415; llarity 27.0%; Pred. No. 2.2e-12; Conservative 33; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 4.
BY SIMILARITY.
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                                                                                                                                          EMBL; U29173; AAA68964.1; -. EMBL; L38423; AAB00846.1; -. EMBL; U30798; AAA81334.1; -. HSSP; O14763; 1D0G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 AA;
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Local St.
67;
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SIGNAL
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REQUENCE FROM N.A.

TISSUE=Mammary gland;

RA

TISSUE=Mammary gland;

RA

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA

RIJECHUL S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA

RA

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA

Raha S.S., McTey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RIChards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz M., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz M., Smailus D.E.,

Roderstion and initial analysis of more than 15,000 full-length

Nord Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99097247; PubMed=9878548;
Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K., Morinaga T., Higashio K.;
Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
-!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for RANKL-mediated osteoclastogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.

    similarity).
    SUBCELLULAR LOCATION: Type I membrane protein (Potential).
    TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
    WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
    SIMILARITY: Contains 4 TNFR-Cys repeats.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                            TISSUENCE FROM N.A.
TISSUE=Fetal liver;
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019046; AAB86810.1; -.
EMBL; BC019185; AAH19185.1; -.
HSSP; P25942; 1CDF.
MGD; MGI:1314891; Thfrsfila.
GO; GO:0007275; P:development; IMP.
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254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA--ECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFNDQ- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STDKCKPWTNCTLLGKLEAHQGTTESDVVC----SSSMTLRRPPKEAQAYLPSLIV
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CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TURE HUMAN STANDARD; PRT; 277 AA.
P25942; Q9BYU0;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
TURESFS OR CD40.
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|LLLFISV--VVVAAIIFGVYYRKGGKALTANLWNWV--------
                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A. BXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 215; DB 1; Length 625; 28.6%; Pred. No. 2.1e-10; Live 27; Mismatches 91; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66621 MW; F8C1872E99511D8E CRC64;
                                                                                                                                 Glycoprotein, Repeat, Signal
GO; GO:0007515; P:lymph gland development; IMP.
GO; GO:0001503; P:ossification; IMP.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR_i 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                               POTENTIAL
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MEDLINE-89356608; PubMed=2475341;
Stamenkovic I., Clark E.A., Seed I
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les 72; Conservative
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134
106
175
494
625 AA;
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CARBOHYD
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ID TNR5 HU
AC P25942

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DT 15-MAY
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As B-lymphocyc and induced by cytokines in carcinomes.;

MROO. 9:100-440[1989]

MROO. 9:100-440[1989]

MROO. 9:100-440[1980]

MROO. 9:100
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TRII HUMAN
Q9Y6Q6;
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ID TR11 HC
AC 09Y606;
DT 16-OCT-
DT 16-OCT-
DT 10-OCT-
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                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH TRAFE.

MEDLINE=98095703; PubMed=9432981;

Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,

Ökumura K., Yamamoto T., Nagaoka H., Takemori T.;

"Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
extracellular signal-regulated kinase (ERK) activity in CD40

signaling along a ras-independent pathway.";
J. Exp. Med. 187:237-244(1998).
                                                                                                                                                                                                                             MEDLINE=98172745; Pubmed=9511754; Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.; "Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5)."; Gene 207:135-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOSTRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
MEDLINE-98266353; PubMed-9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li C., Ni C.Z., Havert M.L., Cabezas B., He J., Kaiser D., Reed J.C. Satterthwait A.C., Cheng G., Ely K.R., "Downstream regulator TANK binds to the CD40 recognition site on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21532985; Pubmed=11675497;
Ferrari S., Giliani S., Insalaco A., Al-Ghonaium A., Soresina A.R.,
Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,
Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
Plebani A.;
Sato T., Irie S., Reed J.C.;
"A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.";
FEBS Lett, 358:113-118(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97189482; PubMed=9037712; Bajorath J., Aruffo A.; "Construction and analysis of a detailed three-dimensional model the ligand binding domain of the human B cell receptor CD40."; Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mutations of CD40 gene cause an autosomal recessive form of immunodeficiency with hyper IgM.";
Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
-!- FUNCTION: Receptor for INFSFS/CD40L.
-!- SUBUNIT: Interacts with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6.
                                                                                                                                     "CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-oligomerization."; Biochemistry 37:11836-11845(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
                                                                                          MEDLINE=98384149; PubMed=9718306;
Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20442386; PubMed=10984535;
Ni C.Z., Welsh K., Leo E., Chiou C.K., Wu H., Reed J.C.,
"Molecular basis for CD40 signaling mediated by TRAF3.";
Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
                                                                           INTERACTION WITH TRAF1; TRAF2; TRAF3 AND TRAF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAF3.
MEDLINE=22000222; PubMed=12005438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-STRUCTURE MODELING OF 24-144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure 10:403-411(2002)
                                                                                                                                                                                                                  INTERACTION WITH TRAFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT HIGM3 ARG-83.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFK-----K 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CEKVGAVQNS--CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGQPNCNICRVCAG 69
                                                                                                                                                                                                                                                                              Isoid=P25942-2; Sequence=VSP 006472, VSP_006473;

-!- TISSUB SPECIFICITY: B-cells and in primary carcinomas.
-!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an autosomal recessive disorder which includes an inability of B cells to undergo isotype switching, one of the final differentiation steps in the humoral immune system, an inability to mount an antibody-specific immune response, and a lack of germinal center formation.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 Y--FRFKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG------QELTKQGCKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 11A precursor
(Receptor activator'of NF-KB) (Ostèoclast differentiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 CPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQ------
Type I membrane protein (isoform I);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 208.5; DB 1; Length 25.7%; Pred. No. 3.2e-10; ative 37; Mismatches 108; Indels
                                                                                                           Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             616 AA.
                                                                                                                                                                                                                       IsoId=P25942-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 NTAAPVQETLHGCQPVTQEDG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL035662; CAC17670.1; -.
EMBL; AJ300189; CAC29424.1; -.
EMBL; BC012419; AAH12419.1; -.
PIR; S04460; A60771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60592; CAA43045.1; -.
EMBL; AL035662; CAC17670.1; -
SUBCELLULAR LOCATION: 1 secreted (isoform II). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1CDF; 01-APR-97.

1FLL; 18-OCT-00.

1LOA; 08-FEB-00.

1CZZ; 26-SEP-01.
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Best Local Similarity
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-!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant bone disorder characterized by focal areas of increased bone remodelling. The osteolytic lesions develop usually in the long bones during early adulthood. FEO is often associated with early onset deafness and loss of dentition.

-!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone 2 (PBB2) [MIM:602080]; also known as familial Paget disease of bone. PDB2 is a bone remodelling disorder with clinical similarities to FEO. Unlike FEO, however, affected individuals have involvement of the axial skeleton with lesions in the spine, pelvis and skull.

-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson D.M.;
"Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause familial expansile osteolysis.";
Nat. Genet. 24:45-48(2000).
-!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for RANKL-mediated osteoclastogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.
-!- SUBCNLT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in skeletal muscle, thymus, liver, colon, small intestine and adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone
                                                                                                                                                                                                                                                                                                                          TISSUE=Dendritic cell;
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The TRAF family of signal transducers mediates NF-kappaB activation
                               номо sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Маmmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_тахID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
ALA-LEU-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
MEDLINE=20082806; Pubmed=10615125;
Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
MEDLINE=98447691; PubMed=9774460;
Wong B.R., Josien R., Lee S.Y., Vologodskaia M., Steinman R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99097247; PubMed=9878548;
Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAF3; TRAF5 AND TRAF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the TRANCE receptor.";
J. Biol. Chem. 273:28355-28359(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF018253; AAB86809.1; -.
receptor) (ODFR).
INFRSF11A OR RANK
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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104
HSSP; P25942; 1CDF.

Genew; HGNC:11908; TNFRSF11A.

R MIM; 603499; -.

R MIM; 174810; -.

R MIM; 602080; -.

R GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0007165; P:signal transduction of cell proliferation; TAS.

GO; GO:0007165; P:signal transduction; TAS.

R GO; GO:0007267; P:cell-cell signaling; TAS.

R PROSITE; PS00652; TNFR C6; 4.

R PROSITE; PS00652; TNFR NGFR 1; 1.

R PROSITE; PS00652; TNFR NGFR 1; 1.

R PROSITE; PS00652; TNFR NGFR 2; 1.

R PROSITE; PS00652; TNFR NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 RFKKFCSSTHNAECECIEGFH----CLGPQCTRCEKDCRPG-----QELTKQG-CKTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 -----NSTTPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAQHPLQLNKDTVCKPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LGTENDO-NGIGVCRPWINCSLDGRSVLKIGTTEKDVVCGPPVVSFSPSTTISVTPEGGP
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CYTOLASMIC (POTENTIAL).
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
CHOROLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGICOLOGIC
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035714; Q9JKR1; Q9JKR2; Q9JKR3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor (Glucocorticoid-induced TNFR-related protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%; Score 205.5; DB 1; Length 616; 29.9%; Pred. No. 1.3e-09; tive 25; Mismatches 71; Indels 47;
                                                                                                                                                                                                                                                                                                                                                       RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_011518.
E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TUMOR NECROSIS FACTOR REC
SUPERFAMILY MEMBER 11A.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                 Disease mutation; Deafness.
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2333
6168
11511
1944
600
600
600
1127
1127
1105
1124
124
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                                                                                                                                                                                                                                                                                                                                                                                               192
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Best Local Simi
Matches 61;
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TR18 MOUSE
ID TR18 M
AC 035714
DT 16-OCT
DT 10-OCT
DE TUMOY
DE (Gluco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial cells and in the regulation of T cell receptor-mediated cell death, Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
TRAF6 (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and
C); secreted (isoform D).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=20256302; PubMed=10798444;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Delfino D., Migliorati G., Riccardi C.;
"Gene structure and chromosomal assignment of mouse GITR, a member of
the tumor necrosis factor/nerve growth factor receptor family.";
DNA Cell Biol. 19:205-217(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytes.
-!- INDUCTION: Upregulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                      Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.;
"A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=035714-4; Sequence=VSP_006509;
TISSUE SPECIFICITY: Preferentially expressed in activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20292073; PubMed=10836847;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino Brunetti L., Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
Cell Death Differ. 7:408-410(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=035714-3; Sequence=VSP_006511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=035714-2; Sequence=VSP_006510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=035714-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A. (ISOFORMS B; C AND D)
                                                                                                                                                                            STRAIN=C3H;
MEDLINE=97322352; PubMed=9177197;
                                                                                                                               [1]
SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A. (ISOFORM A).
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EMBL; AF229432; AAF61566.1; -.
EMBL; AF229433; AAF61567.1; -.
EMBL; AF229434; AAF61568.1; -.
MGD; MGI:894675; Tnfrsf18.
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                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 NAVCIP----EPLPTEQY-----GH----LTVIFLVMAACIFFLTTVQLGLHIWQLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACĪFFLTTVQLGLHIWQLRRQHMCPRETQPFĀEVQLSĀED
ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
-> VLLQRPSHSRRCSCQLRMLAASSSLRRNAGSRQKKSVI
WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETQPFAEVQĽSAEDACSFQFPEEERGEQTEEKCHLGGRWP
-> GQLCPREGENVSQAPHLPQFYYRDPAIRGGAVVS (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 SIGGOPNC-----NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPQCTRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 K-DCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK
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P43489; Q13663;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
receptor; (ACT35 antigen) (TAX-transcriptionally activated
glycoprotein 1 receptor) (CD134 antigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 18. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PON-LINKED (GLC
               PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50D8C275D9C56259 CRC64;
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/FTId=VSP_006509
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SMART; SM00208; INFR; 2.
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                                                                             Receptor; Transmembra
Alternative splicing.
SIGNAL
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CARBOHYD
CARBOHYD
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TNR4 HUMAN
ID TNR4 H
AC P43489
DT 01-NOV
DT 10-OCT
DE TUMOR
DE TECCEPT
DE G1YCOP
GN TNFRSF
OS HOMO S
                                                                                                                                                               CHAIN
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Homo sapiens (Human)

InterPro; IPR006210; IEGF. InterPro; IPR001368; INFR_c6. SMART; SM00181; EGF; 1.

; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryota; Metazoa; NCBI_TaxID=9606;

SEQUENCE FROM N.A.
MEDLINE=94170844; PubMed=7510240;
Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994). SEQUENCE FROM N.A.

MEDLINE=95219871; PubMed=7704935;
Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.; "Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";
Circ. Shock 44:30-34(1994).

SEQUENCE FROM N.A. MEDLINE=20318724; PubMed=10861060; Pankow R., Duerkop H., Latza U., Krause H., Kunzendorf U., Pohl

Bulfone-Paus S.;
"The HTLV-I protein transcriptionally modulates OX40 antigen
expression.";

INTERACTION WITH TRAF1; TRAF2 AND TRAF3.

MEDLINE=98078711; PubMed=9418902;

Arch R.H., Thompson C.B.;

"4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB.";

Mol. Cell. Biol. 18:558-565(1998).

NITERACTION WITH TRAF2 AND TRAF5.

X MEDLINE=98157982; PubMed=9488716;

A Kawamata S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;

Kawamata S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;

Kakivation of Ox40 signal transduction pathways leads to tumor necrosis factor receptor-associated factor (TRAF) 2- and TRAF5-mediated NF-kappaB activation.";

J. Biol. Chem. 273:5808-5814(1998).

CC -!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.

CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

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MIM; 600315; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
GO; GO:0006955; P:immune response; TAS.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
SMART; SM00208; TNFR; 3.

THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC 139 140 SLDGRSVLKTGTTEKDVVC------178 208 EVPGGRAVAAI-LGLGLVLGLLGPLAILLALY-LLRRDQRLPPDAHKPP------254 CHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSER-KQLCTA 101 :| |: |: | : | :| |: | 148 TLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPV --PGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE 28 CDNCQPGT-----PCRKYNPVCKSCPPSTFSSIGGQPNCNICRVC----AGYFRFKKFCSS SUPERFAMILY MEMBER 4.

EXTRACELLULAR (POTENTIAL).

TOTOPLASMIC (POTENTIAL).

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3 (INCOMPLETE).

TNFR-CYS 4.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

4.2%; Score 202.5; DB 1; Length 277; 25.4%; Pred. No. 1e-09; iive 35; Mismatches 94; Indels 59. 29340 MW; 237 DACSCRCPQEEE 248 255 GGGSFŘTPIQÉE 266 64; Conservative 147 146 160 277 AA; Similarity DCMAIN
TRANSMEM
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DISULFID
CARBOHYD
CARBOHYD
SEQUENCE 80 179 43 Query Match Local Best Loc Matches g ð a d g $\stackrel{>}{\circ}$ g ò g ð δ

HUMAN

435 AA STANDARD; HUMAN TNR3 HUN P36941;

01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 3 precursor (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor). Homo sapiens (Human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; SEQUENCE FROM N.A.

ь. : MEDLINE=93252381; PubMed=8486360; MEDLINE=93252381; PubMed=8486360; Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993). TISSUE=Liver;

[2]

Genew; HGNC:1 MIM; 600315;

400208; TNFR; 3. PS00652; TNFR_NGFR_1; 2. PS50050; TNFR_NGFR_2; 2.

Transmembrane, Glycoprotein; Repeat; Signal. 28

Antigen;

Receptor; 1 SIGNAL

CHAIN

TUMOR NECROSIS FACTOR RECEPTOR

מוזה הומא

. H

Immunol. 165:263-270(2000).

EMBL; X75962; CAA53576.1; -.
EMBL; S76792; AAB33944.1; ALT_INIT.
EMBL; AJ277151; CAB96543.1; -.
PIR; I37552; I37552.
HSSP; O14763; ID0G.
Genew; HGNC:11918; TNFRSF4.

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Receptor; ; sIGNAL
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REPEAT
REPEAT
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DISULFID
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DISULFID
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            TISSURE-Lung;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Hoshins R.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Hoshins R.F., Jordan H., Moore T., Mars S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Mars S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J., Usquellano M.F., Perers G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RIChards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

RI human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99223511; PubMed=10207006; Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.; "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell death in HeLa cells."; J. Biol. Chem. 274:11868-11873(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am. J. Pathol. 152:1549-1561(1998).

[8]

INTERACTION WITH TRAFS.

MEDLINE=98172745; PubMed=9511754;

Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.;

"Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAFS).";

Gene 207:135-140(1998).

-! FUNCTION: Receptor for the heterotrimeric lymphotoxin containing if And LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98289299; PubMed=9626059;
Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,
Reynolds A., Clevenger C.V., Reed J.C.;
"TRAF-4 expression in epithelial progenitor cells. Analysis in normal adult, fetal, and tumor tissues.";
Am. J. Pathol. 152:1549-1561(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH TRAF3.

MEDLINE=96278943; PubMed=8663299;

Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,

Yagita H., Okumura K.;

"TRAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor.";

J. Biol. Chem. 271:14661-14664(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=20261554; PubMed=10799510;
Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
"The lymphotoxin-beta receptor is necessary and sufficient for LIGHT-mediated apoptosis of tumor cells.";
J. Biol. Chem. 275:14307-14315(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor."; Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94225209; PubMed=8171323;
SEQUENCE FROM N.A.
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CCCCETTAPARTET

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KRKTOCRCOPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQPN-CNICRVCAGYFRFKKF--CSS
SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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435 TURR-CYS 1.

124 TURR-CYS 2.

168 TURR-CYS 3.

211 TURR-CYS 3.

211 TURR-CYS 4.

58 BY SIMILARITY.

80 BY SIMILARITY.

80 BY SIMILARITY.

116 BY SIMILARITY.

124 BY SIMILARITY.

132 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

148 BY SIMILARITY.

140 N-LINKED (GLCNAC. . .) (POTENTIAL).

177 N-LINKED (GLCNAC. . .) (POTENTIAL).

177 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM, 600979; -. GO: 0007165; P: signal transduction; TAS.

GO: 0007165; P: signal transduction; TAS.

InterPro; IPR008063; Fas receptor.

InterPro; IPR001368; TNFR c6.

Pfam; PF00020; TNFR c6; 4.

PRINTS; PR01680; FASRECEPTOR.

SMART; SM00208; TNFR; 4.

PROSITE; PS00652; TNFR NGFR 1; 2.

PROSITE; PS00050; TNFR NGFR 2; 3.

Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 14.1%; Score 202; DB 1; Length 435; Local Similarity 25.7%; Pred. No. 1.7e-09; es 56; Conservative 26; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPSARCQPHTRCENQGLVBAAPGTAQSDTTCKNPLEPLPPEMSGTM-
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                         -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                 EMBL; L04270; AAA36757.1; -.
EMBL; BC026262; AAH26262.1; -.
PIR; I54182; I54182.
HSSP; P25942; ICDF.
Genew; HGNC:6718; LTBR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20292073; PubMed=10836847;
MEDLINE=20292073; PubMed=10836847;
Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Nocentini G., Ronchetti G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
"Identification of three novel mRNA splice variants of GITR.";
cell Death Differ. 7:408-410(2000).
-!- FUNCTION: Receptor for TNFSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial cells and in the regulation of T cell receptor-mediated cell death.
Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
-!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF5.
                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2 AND
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=T-cell;
MEDLINE=99156876; PubMed=10037686;
Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
Liu D., Wang S.-X., Kwon B.S.;
"Identification of a novel activation-inducible protein of the tumor
necrosis factor receptor superfamily and its ligand.";
J. Biol. Chem. 274:6056-6061(1999).
             TRIB HUMAN STANDARD; PRT; 241 AA.
09Y5<del>U</del>5; 095851; 09NYJ9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
                                                                                                                                                                                                                                                                                                                 and its receptor, a human ortholog of mouse GITR.";
Curr. Biol. 9:215-218(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=99175482; PubMed=10074428;
Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
Ashkenazi A.;
"Identification of a new member of the tumor necrosis factor fan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) Secreted (isoform 2).
ALTERNATIVE PRODUCTS:
Event_Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q9Y5U5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF125304; AAD22635.1; -.
EMBL; AF117297; AAD19694.1; -.
                                                                                                                TNFR family receptor).
TNFRSF18 OR GITR OR AITR.
                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 HNAVCVP------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTENTIAD.

CYTOPLASMIC (POTENTIAL).

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

BY SIMILARITY.

COFFELTIVE GRANTHANOUND SPPAEPLE WILLANDAR CYLLITSAQLGIHIWQLRSQCWWPRETQLLIEVPPSTEDAR SCOFFEERGERSAEEKGRIGDLWV -> CWRCRRRPKTPE AASSPRKSGASDROKRRGWETCGCEFGRPPGPPTAASPSP GAPQAAGALRSALGRALLPWQQKWVQEGGSDQRPGPCSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 cgpgri-ligigidarcckvhttrccrdypgeeccsew---bcmcvopefhcgdpcctrc
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                           C-domain) receptor activity; TAS
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 18.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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SQCMWPRE -> K (IN REF. 2)
90DC3B4AA7E82CBE CRC64;
                                                                                                                                                                                                                                        PROSITE; PSO0652; TNFR NGFR 1; FALSE NEG.
PROSITE; PSS0050; TNFR NGFR 2; FALSE NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Alternative splicing.
SIGNAL 1 25 POTENTIAL.
CHAIN 26 241 TÜMOR NECROSIS FACTOR REC
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28.8%; Pred. No. 2.5e-09;
tive 25; Mismatches 85
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                                                         MIM; 603905; -. GO; GO: 0005027; F:NGF/TNF (6 C-domain) rece GO; GO: 0006916; P:anti-apoptosis; TAS. GO; GO: 0007165; P:signal transduction; TAS. InterPro; IPR001368; TNFR C6. SMART; SM00208; TNFR, 2.
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26000 MW;
EMBL; AF241229; AAF63506.1;
Genew; HGNC:11914; TNFRSF18.
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Best Local Similarity 28.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AA;
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MARTINE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MALSchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Mannan and mouse cDNA sequences.";
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MEDLINE-96299745; PubMed-8661109;
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  NCBI_TaxID=9606;
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171 NTTSSTDICRPHQICNV----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQH 226
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PTM: A soluble form (tumor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing. PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to servere rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portinion of TNFR2 linked to an Immuglobulin Fc chain. It binds to TNFR-alpha and blocks its interactions with receptors. SIMILARITY: Contains 4 TNFR-Cys repeats. DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm". DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrel.com/".
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EMBL; U52165; AAC50622.1; -.
EMBL; U52156; AAC50622.1; JOINED.
EMBL; U52159; AAC50622.1; JOINED.
EMBL; U52159; AAC50622.1; JOINED.
EMBL; U52160; AAC50622.1; JOINED.
EMBL; U52161; AAC50622.1; JOINED.
EMBL; U52161; AAC50622.1; JOINED.
EMBL; U52163; AAC50622.1; JOINED.
EMBL; U52164; AAC50622.1; JOINED.
EMBL; U52164; AAC50622.1; JOINED.
EMBL; AX264804; AAA89052.1; JOINED.
EMBL; BC052977; AAA52977.1; -.
EMBL; BC052977; AAA63262.1; -.
EMBL; A35356; A35356.
PDR; A35356; A35356.
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000330; 060236; Q9UHP4;
28-FEB-2003 (Rel. 41, Created)
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Matches 72; Conserv
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TISSUE=Eye,

XEDLINE=22388257; PubMed=12477932;

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MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung cancer;
MEDLINE=98151033; PubMed=9492069;
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
TNFRSF11B OR OPG OR OCIF.
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MEDLINE=98238645; PubMed=9571159;
Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda Morinaga T., Tsuda E., Higashio K.;
"Characterization of monomeric and homodimeric forms of osteoclastogenesis inhibitory factor.";
Biochem. Biophys. Res. Commun. 245:382-387(1998).
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                                                                                                                                                                                                                      (Human)
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MEDLINE=21355914; PubMed=11505389;

MEDLINE=21355914; PubMed=11505389;

MEDLINE=21355914; PubMed=11505389;

MEGEOPTO activator of nuclear factor-kappaB ligand and steeptor activator of nuclear factor-kappaB ligand and costeopy acceptor for the pathogenesis and reatment of malignant bone diseases.";

Cancer 92:460-470(2001).

List function in osteoclastogenesis. Inhibits the activation of costeoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.

C. SUBUNIT: Homodimer.

C. SUBCILITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow. Detected at very low levels in brain, placenta and skeletal muscle. Highly expressed in fetal kidney, liver and lung.

C. HIGHLY expressed in fetal kidney, liver and lung.

C. HIGHLY holdsylated. Contains sialic acid residues.

C. HIGHLARITY: Contains 2 death domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
MEDLINE=98148058; PubMed=9478964;
Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
Morinaga T., Higashio K.;
"Characterization of structural domains of human osteoclastogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98269100; PubMed=9603945;
Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman
Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
James I.E., Rosenberg M., Lee J.C., Young P.R.;
"Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
J. Biol. Chem. 273:14363-14367(1998).
                                                                                                                  He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.; "Cloning and expression of osteoprotegerin from Homo sapiens."; Acta Biochim. Biophys. Sin. 31:680-684(1999).
                                                                                                                                                                                                                                                                              SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION. MEDLINE=97312536; PubMed=9168977; Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F., Morinaga T., Higashio K.; "Isolation of a novel cytokine from human fibroblasts that specifically inhibits osteoclastogenesis."; Biochem. Biophys. Res. Commun. 234:137-142(1997).
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J. Biol. Chem. 273:5117-5123(1998)
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[6]
SEQUENCE OF 22-393 FROM N.A.
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                            MIN, 602643, -.

R MIN, 602643, -.

R GO, GO:0005125; F:cytokine activity; TAS.

R GO, GO:0005125; F:cytokine activity; TAS.

R GO, GO:0004872; F:receptor activity; TAS.

R GO, GO:000165; P:signal transduction; TAS.

DR GO, GO:0001501; P:skeletal development; TAS.

DR GO, GO:0001368; TNFR_C6.

InterPro; IPR001368; TNFR_C6.

DR Pfam; PF00020; TNFR_C6; 3.

DR SWART; SM00005; DEATH; 1.

DR SWART; SM00005; DEATH; 1.

DR SWART; SM00005; TNFR 4.

DR PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.

DR PROSITE; PS50050; TNFR_NGFR_1; 1.

DR RECEPTOR; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR

FT CHAIN 21 TUMOR NECROSIS FACTOR RECEPTOR
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TO THE MOUSE STANDARD;

AC P275I2; Q99NE0; Q99NE1; Q99NE2; Q99NE3;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2013 (Rel. 42, Last annotation update)

DT TO CT-2013 (Rel. 42, Last annotation update)
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MISSING: ABOLISHES DIMERIZATION
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TNFR-CYS 3.
TNFR-CYS 4.
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MEDLINE=96382484; PubMed=8790348;

MEDLINE=96382484; PubMed=8790348;

A Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,

Yamamoto T., Inoue J.-I.;

Yamamoto T., Inoue J.-I.;

ITRAF5, a novel tumor necrosis factor receptor-associated factor

T family protein, mediates CD40 signaling.";

Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).

- I- FUNCTION: Receptor for TNFSF5/CD40L.

- I- SUBLNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,

TRAF2 AND TRAF6 (By similarity).

C -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV

and V); secreted (isoform II).

C -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5]
INTERACTION WITH TRAF3.
MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM I).
STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93094586; PubMed=1281194;
Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
"Genomic structure and chromosomal mapping of the murine CD40 gene.";
J. Immunol. 149:3921-3926(1992).
(CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).

TNFRSF5 OR CD40.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM I).
MEDLINE=92105763; PubMed=1370315;

Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wideline=21117110; PubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
"Regulation of CD40 function by its isoforms generated through alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=IV;
IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=P27512-5; Sequence=VSP_006476;
-!- SIMILARITY: Contains 4 TNFR-Cyg repeats.
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# # #	EMBL; M83312 EMBL; M94126 EMBL; M94129		AABU8/05.1; AAA37404.1; AAA37404 1TO	Can
			7404.1; JO	JOINED. JOINED.
		01387; CAC	229427.1;	
2 E E		01389; CAC		
K K	EMBL; AJ4	01390; CAC 76; A46476	729430.1; 5.	
0 8 8 8	HSSP; PZ5 MGD; MGI:	942; 1 88336;	£5.	
몺없	InterPro; InterPro;	IPR008063 IPR001368	as rec NFR c6	eptor.
N C	Pfam; PF00020; INFR C6 PRINTS: PR01680; FASRE	0020; TNFR R01680: FA	FR c6; 4.	
ä	SMART; SM	00208; TNE	FR; 4.	
R R	PROSITE; PROSITE;	PS00652; 7 PS50050; 7		
X	Receptor;	Transmembrane	Ψ	; Glycoprotein; Repeat; Signal;
E EI		1 1 1	119	1
ቹ ት	CHAIN	20	289	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5.
i E	DOMAIN	2	193	
E E	TRANSMEM	194 216	215 289	POTENTIAL. CYMODIASMIC (POTENTIAL)
- E	REPEAT	25	60	
FF (REPEAT	₽ 9	103	TNFR-CYS 2.
7 E	REPEAT	104 145	144 187	INFR-CIS 3. INFR-CYS 4.
FT	DISULFID	26	37	
in Fi	DISULFID	38 1-4	15 10 10	BY SIMILARITY. BY SIMILARITY.
i Fi	DISULFID	· φ	77	
FT	DISULFID	8 L 8 R	103	BY SIMILARITY. BY SIMILARITY.
4 E-1	DISULFID	11	116	
H E	DISULFID	112	143	BY SIMILARITY. N-1-INKED (SLONE) (POTENTIAL)
- H - H	VARSPLIC	16	203	SCEDENLEVLOKGTSQTIVICGLKSRMRALLVIPVVMG ->
ው ሙ ሙ				RFKVPDASPAGHSCRDGHPHHHFRGVSLYQKGGQEIKG (in isoform II).
E E		Č	c c	Id=VSP 00
En En En En	VARSPLIC	204	583	
. E. E	VARSPLIC	187	216	GLKSRMRALLVIPVVMGILITIFGVFLYIK -> E (in
<u> </u>				
E E	VARSPLIC	216	234	KKVVKKPKDNEMLPPAARR -> SECSGEEREGGFSPVEPA S (in isoform III)
FT				/FIId=VSP_006477.
EH E	VARSPLIC	235	289	Missing (in isoform III).
	VARSPLIC	216	222	100
ըս ը Մահե	VAPABIT.	.400	680	/FIIG=VSF 006479. Missing (in isoform IV).
- E	VARSPUIC	623	C 0 V	-
SO	SEQUENCE	289 AA;	32111 MW	; C791CB6Ī
O m	Query Match Best Local S	Similarity	13.1%;	Score 186.5; DB 1; Length 289; Pred. No. 2.2e-08;
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δ.	28	CDNCQPGTFCRKY	CRKYD :	
d d	38	CDLCQPGSR	LTSHCTALER	CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTA 97
ò	80	THNAECECI	THNAECECIEGEHCLGPQCTRCEK-	TRCEKDCRPGQELTKQGCKTCSLGTFNDQNGT 130
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Best Local Similarity
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245
              -GVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTL 189
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TISSUE=Lung, and Skin;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                        FLALTSALLLALI -- FITLLFSVLKWIRKKFPHIFKOP -- FKKTTGAAQBEDACSCRCPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99087326;
MEDLINE=99087326;
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
TNFRSF6B OR DCR3 OR TR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20122600; PubMed=10655513;
Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
"Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S., "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis."; J. Biol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matthews L.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000)
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TISSUE=Prostate;
MEDLINE=99253915; Pubmed=10318773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:699-703(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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ID AC 095407

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RGeneration and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
R. "Generation becoy receptor for the cytotoxic ligands TNFS14/LIGHT
C.!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
C.!- SUBCELLULAR LOCATION: Secreted
C.!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
Detected in adult stomach, spinal cord, lymph node, trachea,
spleen, colon and lung. Highly expressed in several primary tumors
from colon, stomach, rectum, esophagus and in SW480 colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TURR-CYS 1.

TURR-CYS 2.

TURR-CYS 3.

TURR-CYS 4.

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 603361; -.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
InterPro; IPR001368; TNFR_C6.
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Pfam; PF00020; TNFR c6; 4.

SMART; SM00208; TNFR; 4.

PROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS50050; TNFR NGFR 2; 2.

PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF104419; AAD03056.1; -
EMBL; AF134240; AAD29688.1; -
EMBL; AF217796; AAF35244.1; -
EMBL; AF217793; AAF33685.1; -
EMBL; AF217794; AAF33686.1; -
EMBL; AL121845; CAC03668.1; -
EMBL; BC017065; AAH17065.1; -
EMBL; BC034349; AAH34349.1; -
HSSP; O14763; 1D0G.
Genew; HGNC:11921; TNFRSF6B.
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32679 MW;
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DISULFID
CARBOHYD
SEQUENCE
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Gaps

26;

13.0%; Score 185; DB 1; Length 300; 28.3%; Pred. No. 3e-08; ive 24; Mismatches 85; Indels

65; Conservative

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(See http://www.isb-sib.ch/announce/
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
   entities requires a license agreement (Gor send an email to license@isb-sib.ch)
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163
181
82
69 N-
195 N-
50319 MW;
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075509; Q96D86;
28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                              COPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIK 227
                                                                                                                                             HNRACRCRIGFFAHAGFCLE-HASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSEQ 167
                                                                  CAQCPPCTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHAT 108
                                                                                                            HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-----CKTCSLGTFN-DQNGTGV 132
                                                                                                                                                                                         ----- VVSFSPSTTISV- 173
                              90
                              ----CRKYNP-VCKSCPPSTFSSIGGQ-PNCNICRV-CAGYFRFKKFCSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor with high affinity for INFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apprototic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=91246168; PubMed=1645445;
Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
"Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                         -----TPEG-GP----GGHSLQV-----LTLFL-ALTSALLLALI 202
                                                                                                                                                                                                                                                                                                MEDLINE=91187885; PubMed=1849278; Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    P25119; P97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 1B
necrosis factor receptor 2) (TNF-R2) (P75).
TNFRSFIB OR TNFR2 OR TNFR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Inds to TRAF2 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                            CRPWINCSLDGRSVLKTGTTEKDVVC----GPP----
                                                                                                                                                                                                                                                                                                                                                                                                                    474
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                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTEND-QNGTGVCRPWTNCSLDGRSVLKTGTTBKDVVCGP--PVVSFSPSTTISVTP--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----BGGP-----BGGP------GGHSLOVLTLFLALTSALLLALTFILL 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 GTFSDTTSSTDVCRPHRICSI----LAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 FCSSTHNAECECIEGFHCL-----GPQCTRCEKDCRPGQELTKQG-----CKTCSL
EMBL; M59378; AAA40463.1; -.

R EMBL; X87128; CAA60618.1; -.

R EMBL; X87128; CAA60618.1; -.

R PIR; B38634; B38634.

R PIR; B38634; B38634.

R PSP; P19438; INCF.

R GO; GO:00007166; P:cell surface receptor linked signal transdu. . .; I GO; GO:00008220; P:nefrosis; IMP.

R GO; GO:0008220; P:nefrosis; IMP.

R GO; GO:0008220; P:nefrosis; IMP.

R GO; GO:0008220; TNFR_C6.

R SMART; SM00208; TNFR; 4.

R PROSITE; PS00652; TNFR_NGFR_1; 2.

R PROSITE; PS0050; TNFR_NGFR_1; 2.

R PROSITE; PS0050; TNFR_OGP.

R PROSITE; PS0050; TNFR_OGP.

R PROSITE; PS0050; TNFR_OGP.

R PROSITE; PS0050; TNFR_OGP.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR RECEPSUPERFAMILY MEMBER 1B.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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462EAE398C4D6563 CRC64;
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RECTISSUE=Brain, and Colon;

RECTISSUE=Brain, and Colon;

RECTISSUE=Brain, and Colon;

RECTISSUE=21886257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., More T., Max S.I., Wang J., Hsieh F. R.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Aria S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., Morban P.J., McKernan K.J., Malek J.A., Gunnarene P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Bulle S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Hakesley R.W., Touchman J.W., Schmutz J., Wayers R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M., S.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

RA Redriguez A.C. Grimwood J., Schmutz J., Warrs R.M.,

R. Generation and initial analysis of more than 15,000 full-length

RT Generation and initial analysis of more than 15,000 full-length

RT Generation sad initial analysis of more than 15,000 full-length

RT Generation sad scilvate NF-kappa-B and JNK and promote apoptosis.

C. -- Submin T. Associates with TRADD.

-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

-- SIMILARITY: Contains I death domain.

-- CHILARITY: Contains I death domain.

-- CHILARIT
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                                                                                                                                                                                                                                                                          MEDLINE=98378343; PubMed=9714541; Pan G., Yu G., Vincenz C., Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.; "Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";
  28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
related death receptor-6) (Death receptor 6).
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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BC010241; AAH10241.1; ALT_INIT.
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EMBL; BC010241; AAH10241.1;
HSSP; O14763; 1D0G.
Genew; HGNC:13469; TNFRSF21.
MIM; 605732;
InterPro; IPR00488; Death.
                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 431:351-356(1998)
                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9606;
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66 TCDKCPAGTYVSEHCINTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 THNAECECIEGEHCLGPQCTRCEXDCRPGQELTKQG-----CKTCSLGTFND-QNGTG 131
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                                                                                                                                                                   Glycoprotein; Repeat; Signal.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Ratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
(POTENTIAL)
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28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryonic intestine;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 180.5; DB 1; Length 655; 32.3%; Pred. No. 1.5e-07; ive 21; Mismatches 71; Indels 17.
                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                              SUPERFAMILY MEMBER 21.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 VCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTIS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48939391C4852A33 CRC64;
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                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
DEATH.
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BY SIMILARITY.
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             Pfam; PF00531; death; 1.
Pfam; PF000531; death; 1.
Pfam; PF00020; TNFR c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50052; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
Receptor; Apoptosis; Transmembrane; Glycc SIGNAL.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
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InterPro; IPR001368; TNFR_c6
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Best Local Similarity
Matches 52; Conserv
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INVOLVED IN DIMERIZATION (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
MW; FECGA31F1D4E573A CRC64;
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30.8%; Pred. No. 1.2e-07;
ive 21; Mismatches 64; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U94330; AAB53707.1; -...
HSSP; P25942; ICDF.
InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_c6.
InterPro; IPR001368; INFR_c6.
Sfam; PF00020; INFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00005; DEATH; 1.
RPOSITE; PS000652; INFR_NGFR_1; 1.
RPOSITE; PS00652; INFR_NGFR_1; 1.
RPOSITE; PS00652; INFR_NGFR_2; 2.
RPOSITE; PS0050; INFR_NGFR_2; 2.
RPOSITE; 
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH 1.
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401 AA;
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101 HNRVČEČE EGRYLELEFČLK-HRSČPPGLGVLQAGTPERNTVČKRČPDGFFSGETSSKAP 159
HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-----CKTCSLGTFNDQNGT-GV 132
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J. Exp. Med. 192:463-474(2000).

I. Exp. Med. 192:474(2000).

I
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STRAIN=BALB/c; TISSUE=Kidney;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽.
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DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.
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STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
MEDLINE=98382527; PubMed=9714833;
Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga 'Higashio K.;
"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
TNFRSF11B OR OPG OR OCIF.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                 Tilb MoUSE Signated)
28-FEB-2003 (Rel. 41, Dast sequence update)
28-FEB-2003 (Rel. 41, Dast sequence update)
28-FEB-2003 (Rel. 41, Dast annotation update)
28-FEB-2003 (Rel. 41, Dast annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor Tumor necrosis factor receptor superfamily member 11B precursor Tumor necrosis factor (Osteoclastogenesis inhibitory factor).
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                                                                                                                                        158
                                                                                                                                                                                                        160 CRKHTNCSSLGLLLIQKGNATHDNVC 185
                                                                                                                                        CRPWINCSLDGRSVLKTGTTEKDVVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of bone density.";
Cell 89:309-319(1997).
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           estrogens. Downregulated by
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R EMBL; AB013898; BAA33388.1; -.
R EMBL; AB013909; BAA33388.1; -.
R EMBL; AB013900; BAA33388.1; JOINED.
R EMBL; AB013901; BAA33388.1; JOINED.
R EMBL; AB013902; BAA33388.1; JOINED.
R EMBL; AB013902; BAA33388.1; JOINED.
R EMBL; AB013902; BAA33388.1; JOINED.
R HSSP; P25942; ICDF.
R GO; GO:0005578; C:extracellular matrix; IDA.
R GO; GO:0005578; C:extracellular matrix; IDA.
R HSP; P25042; TNFR C6.
R GO; BAA33388.1; JOINED.
R HSSP; P25042; TNFR C6.
R GO; GO:0005578; C:extracellular matrix; IDA.
R PROSITE; PS50017; DEATH; 1.
R PROSITE; PS50050; TNFR NGFR 1; 1.
R PS5005050; TNFR NGFR 1; 1.
R PS5005050; TNFR NG
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30.1%; Pred. No. 1.8e-07;
tive 21; Mismatches 65; Indels 16; Gaps
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CHANKED (GLCNAC. . . ) (ENTRY COLUNKED (GLCNAC. . . 
INDUCTION: Upregulated by TGF-beta and estrogens. 1,25-dihdroxyvitamin D3 and parathyroid hormone. SIMILARITY: Contains 4 TNFR-Cys repeats. SIMILARITY: Contains 2 death domains.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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DEATH 2.
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CDNCQPGTFCRXY----NPVCKSCPPSTFS-SIGGQPNCNICR-VCAGYFRFXKFCSST 80

44; Conservative

Matches

28

Local Similarity

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41 CDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRT 100
                                                                                HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-----CKTCSLGTFNDQNGT-GV 132
                                                                                                                             MEDLINE=SAIN,

WEDLINE=SAIN,

REDLINE=22388257; Pubmed=12477932;

RIAUSDETG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIAUSDETG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIAUSDET R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Cervical adenocarcinoma;
MEDLINE=97053782; PubMed=8898196;
Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
"Herpes simplex virus-1 entry into cells mediated by a novel member of the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        092956; QBWXR1; Q96J31; Q9UM65;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor
Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97306336; PubMed=9162061;
Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
Porter T.G., Truneh A., Young P.R.;
"A newly identified member of the tumor necrosis factor receptor
superfamily with a wide tissue distribution and involvement in
lymphocyte activation.";
J. Biol. Chem. 272:14272-14276(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L., Spear P.G.;
"Search for polymorphisms in the genes for herpesvirus entry Nectin-1, and Nectin-2 in immune seronegative individuals.";
J. Infect. Dis. 185:36-44(2002).
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Zhang W., Wan T., Cao X.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
MEDLINE=21629477; PubMed=11756979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 AA.
                                                                                                                                                                                                                                                                                          160 CIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                    133 CRPWTNCSLDGRSVLKTGTTEKDVVC
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TNFRSF14 OR HVEM OR HVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:11912; INFRSF14.

MIM; 602746; -.

GO; GO:0005027; F:NGF/INF (6 C-domain) receptor activity; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.

GO; GO:0006955; P:immune response; TAS.

InterPro; IPR008063; Fas_receptor.

InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                 HVeA.";

MO1. Cell 8:169-179(2001).

-!- FUNCTION: Receptor for INFSF14/LIGHT and homotrimeric

TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays an important role in HSV pathogenesis because it enhanced the entry of several wildtype HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated human T cells.
-!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                                                                                                                                                                                                                                                   "Herpesvirus entry mediator, a member of the tumor necrosis factor receptor (TNFR) family, interacts with members of the TNFR-associated factor family and activates the transcription factors NF-kappaB and AP-1."; J. Biol. Chem. 272:14029-14032(1997).
                                                                                                      INTERACTION WITH TRAF2 AND TRAF5.
MEDLINE=97298041; Pubmed=9153189;
Hsu H., Solovyev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
"ATAR, a novel tumor necrosis factor receptor family member, signals through TRAF2 and TRAF5.";
U. Biol. Chem. 272:13471-13474(1997).
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SIGNAL.
                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
MEDLINE=21403268; PubMed=11511370;
Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
Eisenberg R.J., Wiley D.C.;
"Herpes simplex virus glycoprotein D bound to the human receptor
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                 INTERACTION WITH TRAF3 AND TRAF5.
MEDLINE=97306297; PubMed=9162022;
Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
Ashkenazi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U81232; AAD00505.1; -.
EMBL, AF153978; AAF75588.1; -.
EMBL, AF373877; AAL47717.1; -.
EMBL, AF373878; AAL47718.1; -.
EMBL, BC002794; AAH02794.1; -.
PDB; 1JMA; 26-SEP-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR c6; 3.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U70321; AAB58354.1; -.
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83 YIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F-SSIGGOPNCNICRVC--AGYFRFKKFCSSTHWAECECIEGFHCL---GPQCTRCE--K 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGNNCYNVVVIVLLLVGCEK----VGAVQNSCDNCQPGTFCRK----YNPVCKSCPPST
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ID _TNR4_RAT

STANDARD; PRT; 271 AA.

AC P15725;

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-APR-1990 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT Tumor necrosis factor receptor superfamily member 4 precursor (OX40L)

DE receptor) (OX40 antigen) (MRC OX40).

CAN TNFRSF4 OR TXGP1L OR OX40.

CAN TNFRSF4 OR TXGP1L OR OX40.

CAN TART STANDARD; Craniata; Buteleostomi;

CAN Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 176.5; DB 1; Length 283; ilarity 29.9%; Pred. No. 1.4e-07; Conservative 18; Mismatches 66; Indels 31;
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 DCRPGQELTKOG-----CKTCSLGTFNDQNGTGVCRPWTNCS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 ISSPGÓRVQXGGTESQDTLCQNCPPGTPSPNGTLEECOHQTKCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30392 MW; 46CE13C2C70242C1 CRC64;
                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
K -> R (in dbSNP:4870).
/FTId=VAR_013007.
                                                                                                                                                                                                                                                                                                                                                   FTId=VAR 013440
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNCTION
                                                                                                                                                                                                 "Mouse
                                                                                                                                                                                Isogai
Minami
                         RESULT 21
TR21_MOUSE
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PVVSFSPSTTISVTPEG------GPGGHSLQVLTLFLAL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GQPNCNICRVC--AGYFRFKKFCSSTHNAECECIEG-----FHCLGPQCTRCEKDCRP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 GQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVGCE----KVGAVQNS-----CDNCQPG----TFC-RKYNPVCKSCPPSTFSSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                    lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
-!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
-!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                           MEDLINE=90214614; PubMed=2157591;
Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive
                                                                                                                                                                                                                               PIR; S12(02)
HSSP; 014763; 1D4V.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6; 3.
SMART; SM00208; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
I 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 170.5; DB 1; Length 271;
; Pred. No. 4.2e-07;
19; Mismatches 83; Indels 79;
                                                                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER 4.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (PO
C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
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TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
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24.6%;
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                                                                                                                                                                                                                                                                                                                            271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                          SEQUENCE FROM N.A.
        NCBI_TaxID=10116;
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236
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Best Local 9
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RESULT 22

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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                        250 AA
                                                                                                                                                     STANDARD;
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2503
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1104
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                                   170 TISVTPEG 177
                                                       | |:|
245 TYE--PQG 250
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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TNR7_MOUSE
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG-----CKTCSLGTFND-QNGTG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 VCRPWTNCSLDGRSVLKTGTTEKDVVCG------PP---VVSFS-------PST 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 SCDNCQPGTFCRKYNP----VCKSCPPSTFS-SIGGQPNCNIC-RVCAGYFRFKKFCSS 79
T-cells, B-cells and monocytes. In T-cells expression is highest in Th0 cells, intermediate in Th2 cells and lower in Th1 cells. SIMILARITY: Contains 4 TNFR-Cys repeats. SIMILARITY: Contains 1 death domain. CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
                                                                                                                                                                                         CC EMBL; AF322069; AAG38115.1; ...

DR EMBL; AF322069; AAG38115.1; ...

DR EMBL; AV043489; AAK74193.1; ...

DR HSSP; O14763; 1D0G.

DR MGD; MGI:2151075; Thfrsf21.

DR InterPro; IPR000488; Death.

DR Pfam; PF00020; TNFR_C6.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00005; DEATH; 1.

DR PROSITE; PS50017; DEATH DOMAIN; 1.

DR PROSITE; PS50050; TNFR, 4.

DR PROSITE; PS50050; TNFR, 4.

DR PROSITE; PS50050; TNFR, 1.

THOMAL I POTENTIAL.

THOMAN HARD NEATHAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 EXTRACELLULAR (POTENTIAL).

570 POTENTIAL.

571 EXTRACELLULAR (POTENTIAL).

572 CYTOPLASMIC (POTENTIAL).

573 TNFR-CYS 1.

574 TNFR-CYS 1.

575 TNFR-CYS 2.

576 TNFR-CYS 3.

577 TNFR-CYS 3.

578 SIMILARITY.

578 BY SIMILARITY.

578 BY SIMILARITY.

578 BY SIMILARITY.

578 BY SIMILARITY.

570 N-LINKED (GLCNAC. .) (POTENTIAL).

570 N-LINKED (GLCNAC. .) (POTENTIAL).

571 N-LINKED (GLCNAC. .) (POTENTIAL).

572 N-LINKED (GLCNAC. .) (POTENTIAL).

573 N-LINKED (GLCNAC. .) (POTENTIAL).

574 N-LINKED (GLCNAC. .) (POTENTIAL).

575 N-LINKED (GLCNAC. .) (POTENTIAL).

576 N-LINKED (GLCNAC. .) (POTENTIAL).

577 N-LINKED (GLCNAC. .) (POTENTIAL).

578 N-LINKED (GLCNAC. .) (POTENTIAL).

579 N-LINKED (GLCNAC. .) (POTENTIAL).

570 N-LINKED (GLCNAC. .) (POTENTIAL).

571 N-LINKED (GLCNAC. .) (POTENTIAL).

572 N-LINKED (GLCNAC. .) (POTENTIAL).

573 M-> I (IN REF. 3).

574 N- I (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 21.
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Best Local Similarity 29.3.3
Laber 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE=93209296; PubMed=8384562;
MEDLINE=93209296; PubMed=8384562;
Gravestein L.A., Blom B., Nolten L.A., de Vries E., van der Horst G., Ossendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Comparison With 4-1BB,
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Comparison W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., Loenen W.A.;
Cosendorp F., Borst J., Loenen W.A.;
Cosendorp F., L
185 KCKAHTDCLGQNLEVVKPGTKETDNVCGMRLFFSSTNPPSSGTVTFSHPEHMESHDVPSS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L24495; -; NOT_ANNOTATED_CDS.

R PIR; A49053; A49053.

R HSSP; P19438; INCF.

RGD; MGI:88326; Tnfrsf7.

RGD; GO:0005515; F:protein binding; IPI.

R GO; GO:0005515; F:protein binding; IPI.

R InterPro; IPR008063; Fas receptor.

R InterPro; IPR001368; TNFR_C6.

R Pfam; PF00020; TNFR_C6.

R PRINTS; PR00208; TNFR_CF.

R SWART; SM00208; TNFR_NGFR_1; 1.

R PROSITE; PS50050; TNFR_NGFR_2; 1.

R Apoptosis; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

T CHAIN 21 250 TUMOR NECROSIS FACTOR RECEPTOR

T DOWAIN 21 182 EXTRACELULAR (POTENTIAL).

T DOMAIN 21 182 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 7 precursor (CD27L receptor) (T-cell activation antigen CD27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . . . .
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SEQUENCE FROM N.A., AND VARIANT THR-59.
MEDLINE=93094588; PubMed=1334106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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TNFRSF7 OR CD27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNR7_HUMAN
ID TNR7_HUMAN
AC P26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                   DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
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REPEAT
DISULFID
DISULFID
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DISULFID
CARBOHYD
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                                                                             SIGNĀL
CHAIN
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         STILLE SELLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
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                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                  80 THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC 139
                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                             140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLL 199
                                                                                                                                                                                                                                                                                             9
8
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                                                                                                                                                                                                                                                                                            CRMCBPGTPFVKDCBQDRTAAQCDPCIPGTSFSPDYHTRPHCBSCRHCNSGFLIRN-CTV
                                                                                                                                                                                                                                                                                                                                                           145 -----LPHGTEXPSW----PLHRQLPNSTVYSQRSSHRPLCSSDCIRIFVTFSSMFLI
                                                                                                                                                                                                                                                       28 CDNCQPGTF----CRXYNPV--CKSCPPST-FS-SIGGQPNCNICRVCAGYFRFKKFCSS
                                                                                                                                                                                                                    Gaps
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

"TINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
TNFRSF5 OR CD40.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - FUNCTION: Receptor for TNFSF5/CD40L.
-! - SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97281252; PubMed=9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                    45;
                                                                                                                                                                              DB 1; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 ALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG
                                                                                                                                                                                                                   94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).-!- SUBCELLULAR LOCATION: Type I membrane protein.-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                           ; Score 169.5; DB 1; Pred. No. 4.7e-07; 29; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; INFR_c6.
   81 BY
96 BY
104 BY
117 BY
120 BY
95 N-
162 N-
28164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                              11.9%;
27.0%;
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PRINTS; PR01680; FASRECEPTOR.
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                        250 AA;
                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNR5 BOVIN
Q28203;
                                                                                                                                                                                                                    62;
                    DISULFID
DISULFID
DISULFID
                                                                             DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                             40
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Best Local
      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 NTDTICVCVEGQHCTSHTCESCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 TGVCRPWINCSLDGRSVLKTGTIEKDVVCGPPVVSFSPSTIISVTPEGGPGGHSLQVLTL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 CDLCPPGQKLVNDCTEVSKTECQSCGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 FEKCHRWISCERKGLVEQHVGINKIDVVCG----FQSRMRILVVIP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGQPNCNICRVCAGYFRFKKFCSSTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 FLALTSALLILALIFIT-LLFSVLK------WIRKKFP-----HIFKOPFKKTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (Rel. 23, Last sequence update)
3 (Rel. 42, Last annotation update)
osis factor receptor superfamily member 7 precursor (CD27L
(T-cell activation antigen CD27) (T14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Monocytes;
MEDLINE=92013149; PubMed=1655907;
Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
"The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor gene family.";
J. Immunol. 147:3165-3169(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 167; DB 1; Length 269; Similarity 25.5%; Pred. No. 8e-07; Conservative 28; Mismatches 94; Indels
                                                                                                   NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
                                                                                                                       SUPERFAMILY MEMBER 5.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     746903F30F95F387 CRC64;
                                                 Receptor, Transmembrane; Glycoprotein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 AA
PROSITE; PS50050; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29983 MW;
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01-AUG-1992 (Rel. 23, Last seq
10-OCT-2003 (Rel. 42, Last ann
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>269
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187
37
37
59
77
103
119
116
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MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH SIVA.

INTERACTION WITH SIVA.

TISSUB=Cervical carcinoma, and Thymus;

MEDLINE=97322375; PubMed=9177220;

MEDLINE SIVA;

MEDLINE And binds to Siva, a proapoptotic protein.";

Proc. Natl. Acad. Sci. U.S.A. 94:6346-6351(1997).

MEDLINCTION: Receptor for TNFSF7/CD27L. May play a role in survival of activated T-cells. May play a role in apoptosis through association with SIVA.

MEDLINE: SUBCELLULAR LOCATION: Type I membrane protein.

MEDLINE SPECIFICITY: Found in most I lymphocytes.

MEDLINCARITY: Contains 3 TNFR-Cys repeats.

MEDLIARITY: Contains 3 TNFR-Cys repeats.

MEDLIARITY: Contains 3 TNFR-Cys repeats.

MEDLIARITY: May NOTE=CD guide CD27 entry;

MWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                        Borst J.;
"The TNF receptor family member CD27 signals to Jun N-terminal kinase
via Traf-2.";
              dorst J.;
'Genomic organization and chromosomal localization of the human CD27
 Loenen W.A., Gravestein L.A., Beumer S., Melief C.J., Hagemeijer A.,
                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH TRAF2.
MEDLINE=98355639; PubMed=9692890;
Gravestein L.A., Amsen D., Boes M., Calvo C.R., Kruisbeek A.M.,
                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 186711; -.
GO; GO:0005886; C:plasma membrane; TAS.
InterPro; IPR008063; Fas_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 28:2208-2216(1998).
                                                Immunol. 149:3937-3943(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M63928; AAA58411.1; -. EMBL; BC012160; AAH12160.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A46517; A46517.
HSSP; P19438; INCF.
                                                                      SEQUENCE FROM N.A.
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 -------TSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 TANAECACRNGWOCRDKECTECD------------PLPNP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPSTT----ISVTPEGGPGGHSLQVLTLFLAL-- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 CQMCEPGTFLVKDCDQHRKAAQCDPCIPGVSFSPDHHTRPHCESCRHCNSGLLVRN-CTI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 CDNCQPGTF----CRKYNPV--CKSCPPS-TFS-SIGGQPNCNICRVCAGYFRFKKFCSS
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PROSITE; PS50050; TNFR_NGFR_1; 1.
Apoptosis; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Phosphorylation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 166.5; DB 1; Length 260; 25.0%; Pred. No. 8.5e-07; tive 25; Mismatches 85; Indels 79
                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 7.
                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POT
PHOSPHORYLATION (POTENTIAL)
A -> T (in dbSNP:758738).
                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                "TId=VAR 016148.
43C38B9ZFA90D4E2 CRC64;
                                                                                                                                                                                                              TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AA
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                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.v.,
Thes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 SCR--CPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 PCRYSCPREEEG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor) (OX40 antigen). TNFRSF4 OR TXGP1 OR OX40.
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                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA;
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TNR4_MOUSE
ID _TNR4_MOUSE
                                                                                                                                                                     DOMAIN
TRANSMEM
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TISSUE=Brain;
MEDLINE=21456161; PubMed=11572484;
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    72 VNYDTCKQCTQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Je proteins.";
Res. 8:179-187(2001).
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                                                                                                   161 -----
                                                                                                                                                                                                                 HUMAN
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                                                                                                                                                                              RESULT 26
LMAS HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 VVVIVLLLVGCEKVGAVQNS-----CDNCQPG----TFC-RKYNPVCKSCPPSTFSSI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Gaps
                                                                                                                                                              Barclay A.N.;
"Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
-!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
-!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
-!- SUBCELULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
MEDLINE=94044750; PubMed=822823;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 221674; CAA79772.1; -.

R EMBL; X85214; CAA59476.1; -.

R PIR; 148700; 148700.

R HSSP; O14763; 1D0G.

R MGD; MGI:104512; Tnfrsf4.

R GO; GO:0005886; C:plasma membrane; IDA.

R MGD; MGI:104512; Tnfrr Go; 3.

R MART; SM00208; TNFR Co; 3.

R PROSITE; PS00652; TNFR NGFR 1; 2.

R PROSITE; PS50050; TNFR NGFR 1; 2.

R Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.

R SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. . .) (POTENTIAL) .
N REF. 2) .
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EXTRACELLULAR (POTENTIAL).
                                                                                                             SEQUENCE FROM N.A.
MEDLINE=95255413; PubMed=7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; Indels
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06E7BB4156F0D08E CRC64;
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TNFR-CYS 2.

TNFR-CYS 3 (INCOMPLETE).

TNFR-CYS 4.

BY SIMILARITY.

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; Pred. No. 4.5e-06;
25; Mismatches 87;
                                                                                 J. Immunol, 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
30153 MW;
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Best Local Similarity 23.89
Matches 57; Conservative
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RX PEQUENCE FROM N.A.

RX PEQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDINDS=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,

RA Jones M., Stavides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Brown A.J.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Colley V.E., Coller R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Slington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Filington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

Ry Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Ry Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Ry Hilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Williams S.,

Ry Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
---NHRSGSELKQ--NCTPTQDTVCR--CRPGTQPRQDS 115
                                                                        GYKLGVDCVPCPPGHFSPGNNQ-ACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLL 174
                                                                                                                                                                                   175 WETQRPTFRPTTVQSTTVWPRTSELPSPPTLVTPEGPAFAVLLGLGLGLLAPLTVLLAL 233
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                                                                                                                                        --- PVVSFSPSTTISVTPEG-----GPGGHSLQVLTLFLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:31-39(1998).
                                            -----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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MEDLINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                         015230; Q8WZA7; Q9H1P1;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Laminin alpha-5 chain precursor.
LAMA5 OR KIAA0533 OR KIAA1907.
                                                                                                                                                                                                                                                                                                          3695 AA.
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PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01248; LAMININ TYPE EGF; 19.
PROSITE; PS50025; LAM G DOMAIN; 5.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
1 35 POTENTIAL.
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Best Local Similarity 28.2%;
Matches 51; Conservative
                                                                          1638
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                                                                                                                            EXPESSION IN RETINA.

REPERSON IN RETINA.

MEDLINE=20422761; PubMed=10964957;

MEDLINE=20422761; PubMed=10964957;

MEDLINE=20422761; PubMed=10964957;

MEDLINE=20422761; PubMed=10964957;

RA ALIBDY R.T., Champliand M.-F., Claudepierre T., Xu Y., Gibbons E.P.,

Koch M., Burgesson R.E., Hunter D.D., Brunken W.J.;

"Laminin expression in adult and developing retinae: evidence of two

RT novel CNS laminins.";

J. Neurosci. 20:6517-6528(2000).

C.: FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the atrachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

C.:-FUNCTION: Laminin-15 complex is an heterotrimer composed of three chains (alpha-5/beta-2/gamma-3) which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.

C.:-SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).

C.:-TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal muscle, pancreas, retina and placenta. Little or no expression in brain and liver.
                                                                                                                                                                                                                                                                                                                                                         brain and liver.

DOMAIN: Domain G is globular and is part of the major cell-binding site located in the long arm of the laminin heterotrimer.

SIMILARITY: Contains 1 laminin N-terminal domain.

SIMILARITY: Contains 22 laminin EGF-like domains.

SIMILARITY: Contains 2 laminin IV domains.

SIMILARITY: Contains 5 laminin G-like domains.
                                   TISSUE-Placenta;
MEDLINE-97415425; PubMed-9271224;
Durkin M.E., Loechel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
                                                                    "Tissue-specific expression of the human laminin alpha5-chain, and mapping of the gene to human chromosome 20q13.2-13.3 and to distal mouse chromosome 2 near the locus for the ragged (Ra) mutation."; FEBS Lett. 411:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR0080985; ConA like_lec_gl.
InterPro; IPR008212; Lam_N2.
InterPro; IPR00034; Laminin_B.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL354836; CAC22309.1; ALT_SEQ.
EMBL; AL354836; CAC22310.1; -.
EMBL; AB067494; BAB67800.1; -.
EMBL; AB011105; BAA25459.1; -.
EMBL; Z95636; CAB09137.1; -.
HSSP; P02468; IKLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00052; laminin B; 1.
Pfam; PF00054; laminin B; 1.
Pfam; PF00054; laminin G; 2.
Pfam; PF00055; laminin Nterm; 1.
PRINTS; PR00011; EGFLAMININ.
ProDom; PD002082; Lam N2; 1.
ProDom; PD003031; Laminin B; 1.
SMART; SM00180; EGF Lam; 20.
SMART; SM00281; LamB; 1.
           [4]
SEQUENCE OF 2743-3695 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00180; EGF Lam; 20.
SMART; SM00281; LamB; 1.
SMART; SM00282; LamG; 5.
SMART; SM00136; LamMT; 1.
PROSITE; PS00022; EGF_1; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:6485; LAMA5.
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LAMININ ALPHA-5 CHAIN.
LAMININ ALPHA-5 CHAIN.
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
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LAMININ GF-LIKE 22.
LAMININ GF-LIKE 31.
LAMININ GF-LIKE 22.
LAMININ GF-LIKE 31.
LAMININ GF-LIKE 41.

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11;
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                                                           KVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKFC--
                              Gaps
DB 1; Length 3695;
                              Indels
Score 141.5; DB Pred. No. 0.0013;
                              9; Mismatches
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LAMININ G-LIKE 5.
COLLED COIL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
ELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.

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PTM: Phosphorylated on serine residues.
                                                                                                                                                                                                                                                                                                                         L Similarity 27.6 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
                                      43
64
82
106
1123
1164
1164
1005
2005
323
323
343;
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TR16_CHICK
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DC TO1-NOV.
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 183
                                                       ----SSTH--NAECECIEGFHCLGPOCTRCEKDCRPGQ-ELTKOGCKTCSLGTFNDQNGT 130
                                                                                                                                GVCRPWT---NCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTIS----VTPEGGPGGHS
                                                                                                                                                                      -----PPGLSGERCDTCSQQHQVPVPGGPVGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=87321103; PubMed=2820128;
Upton C., Delange A.M., McFadden G.;
"Tumorigenic poxviruses: genomic organization and DNA sequence of the
telomeric region of the Shope fibroma virus genome.";
Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91207415; PubMed=1850261;
Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
"T2 open reading frame from the Shope fibroma virus encodes a soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M17433; -; NOT ANNOTATED CDS.

EMBL; M23727; CAA01687.1; -.

PIR; B43692; B43692.

HSSP; P19438; 1EXT.

InterPro; IPR001368; TNFR.c6.

Pfam; PF000208; TNFR.c6; 2.

SMART; SM002089; TNFR.1; 2.

PROSITE; PS00652; TNFR.MGFR.2; 1.

PROSITE; PS00650; TNFR.MGFR.2; 1.

Receptor; Glycoprotein; Repeat; Signal.

SIGNAL 1 16

CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
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F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shope fibroma virus (strain Kasza) (SFV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 176:335-342(1991).
-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF PRACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor soluble receptor precursor (Protein T2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the TNF receptor.";
2122 GRCDPHTGRCNC----
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
325
62
104
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leporipoxvirus.
NCBI_TaxID=10272;
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27
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P25943;
                                                         78
                                                                                           2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
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Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
"Structure and developmental expression of the chicken NGF receptor.";
Dev. Biol. 137:287-304(1990).
-!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
and NT-4. Can mediate cell survival as well as cell death of
neural cells (By similarity).
-!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
associated cell death executor. Interacts with TRAF2, TRAF4,
TRAF6 and PTPN13 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNCOPGTFCRKY----NPVCKSCPPSTF-SSIGGOPNCNICR-VCAGYFRFKKFCSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 CASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLSESQPCDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
Shooter E.M., Reichardt L.F.;
"Structure and developmental expression of the nerve growth factor
receptor in the chicken central nervous system.";
Neuron 2:1123-1134 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor (Lo affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(P75 ICD) (Low affinity neurotrophin receptor p75NTR).
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%; Score 140.5; DB 1; Length 325; 27.6%; Pred. No. 0.00015; tive 12; Mismatches 54; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PO 810530339198A71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 ---SLDGRSVLKTGTT--EKDVVCGPPVVSFSPSTT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AGYGVSGHT--RAGDTLCEK---CPPHTYSDSLSPT 161
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28-FEB-2003 (Rel. 41, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein
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                                                                                                                                                                                                                                                                                                                                                                                       protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                               Variola virus.
Viruses, dsDNA viruses, no
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U18341; AAA69467.1
                                                                               G2R OR G4R
                                                                                                                                                                                        NCBI_TaxID=10255;
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U88152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PVCKSCPP 49
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                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 3.
PROSITE; PS50017; DEATH DOMAIN; 1.
Receptor: Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 9.8%; Score 139.5; DB 1; Similarity 25.7%; Pred. No. 0.00022; 53; Conservative 24; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 VVIVLLLVGCEKVGAVQNSCDNC-----QPGTFCRKYN
SIMILARITY: Contains 4 TNFR-Cys repeats. SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA
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SER/THR-RICH.
BY SIMILARITY.
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C -> Y (IN REFT OF COLON.)
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                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                             PIR; JN0006; JN0006.
HSSP; P07174; INGR.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
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416 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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STRAIN=Garcia-1966;
MEDLINE=20107289; PubMed=10639322;
Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
Esposito J.J.;
"Alastrim smallpox variola minor virus genome DNA sequences.";
Virology 266:361-386(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN=Garcia-1966, and Somalia-1977;
Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contribute to
RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter C.J.;
"Potential virulence determinants in terminal regions of variola smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
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STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
Loparev V.N., Parsons J.M., Esposito J.J.;
Loparev V.N., Parsons J.M., Esposito J.J.;
"DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contrib the modification of TNF-mediated antiviral processes (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.
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Page 30

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H -> Y (IN STRAINS BUTLER-1952, GARCIA-1966 AND SOMALIA-1977).
A -> T (IN STRAINS BUTLER-1952 AND GARCIA-1966).
E -> K (IN STRAIN SOMALIA-1977).
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(POTENTIAL).
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A -> E (IN STRAIN SOMALIA-1977).
N -> D (IN STRAINS BUTLER-1952 AND GARCIA-1966).
P -> L (IN STRAINS BUTLER-1952 AND
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TUFR-CYS 1.
TUFR-CYS 2.
BY SIMILARITY.
CONTRIBUTY.
CONTR
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       PIK; D30000; D3175.

PIR; D72175; D72175.

PIR; D72175; D72175.

HSSP; O14763; 1D603.

HSSP; O14763; 1D607.

INTERPO; IPR001368; TNFR C6.

PFam; PF00020; TNFR C6; 2.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR NGFR 1; 2.

PROSITE; PS50050; TNFR NGFR 2; 2.

Receptor; Glycoprotein; Repeat; Signal.
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GARCIA-1966)
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  D36858;
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ID LMA2_M
AC Q60675
DT 01-NOV
DT 15-MAR
DE LAMINI.
DE Chaini.
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MEDLINE=20085745; PubMed=10619025;

WEDLINE=20085745; PubMed=10619025;

The crystal structure of a laminin G-like module reveals the molecular basis of alpha-dystroglycan binding to laminins, perlecan, and agrin.";

The crystal structure of a laminin G-like module reveals the molecular basis of alpha-dystroglycan binding to laminins, perlecan, and agrin.";

Mol. Cell 4:783-792(1999).

L. FUNCTION: Binding to cells via a high affinity receptor, laminin is cells into tissues during embryonic development by interacting with other extracellular matrix components.

C. -- SUBUNIT: Laminin is a complex glycoprotein, consisting of three comprising one long and three short arms with globules at each each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. The alpha-2 chain is a subunit of laminin-2 (Merosin) and laminin-4 (S-merosin). Interacts with FBLN1, FBLN2 and NID2.

--- SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure. DOMAIN: Domains VI, IV and G are globular. DISEASE: Defects in LAMA2 are a cause of murine muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 20-25.
MEDLINE=21818471; PubMed=11829758;
Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
"Complete sequence, recombinant analysis and binding to laminins and sulphated ligands of the N-terminal domains of laminin alpha3B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 64-281 FROM N.A.
MEDLINE=95179178; PubMed=7874173;
Xu H., Wu X.R., Wewer U.M., Engvall E.;
"Murine muscular dystrophy caused by a mutation in the laminin alpha
             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING TO FBLN1, FBLN2, AND NID2.
MEDLINE=99146904; PubMed=10022829;
Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
"Binding of the G domains of laminin alphal and alpha2 chains ar perlecan to heparin, sulfatides, alpha-dystroglycan and several extracellular matrix proteins.";
EMBO J. 18:863-870(1999).
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                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6, TISSUE=Thymus;
MEDLINE=93346725; PubMed=8345183;
Chang A.C., Wadsworth S., Coligan J.E.;
"Expression of merosin in the thymus and its interaction with
                                                                                                                                                                                                            "Cloning and expression of laminin alpha 2 chain (M-chain) mouse.";
                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Embryo, and Heart;
MEDLINE=95316259; PubMed=7795883;
Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 laminin N-terminal domain. SIMILARITY: Contains 17 laminin EGF-like domains.
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                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2162-2279 FROM N.A.
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                                                                                                                                                                                                                                                                   Matrix Biol. 14:447-455(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (Lama2) gene.";
Nat. Genet. 8:297-302(1994).
                                                                           WCBI TaxID=10090;
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23 AVQNSCDN-----CQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKK
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925 DC-HTRIGQCECRPNVQGRHCDECKPETFGLQLGRGCLPCNCNSFGSKSFDCEASGQCWC
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Best Local Similarity 26.7%; Pred. No. 0.0022;
Matches 54; Conservative 19; Mismatches 67; Indels 6
(POTENTIAL)
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 EMBL; X69869; CAA49202.1; ---
DR EMBL; X67315; AAA5302.1; ---
DR EMBL; X67315; AAA3373.1; ---
DR PRB; 14907; S3386.

PDB; 10V0; 03-DEC-99.

PDB; 10V0; 03-DEC-99.

PDB; 10V0; 03-DEC-99.

RGD; GO:0005604; C:basement membrane; IDA.

RGD; GO:0005604; C:basement membrane; IDA.

RICEPPO; IPRO00899; EGF Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ike | Ik
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LAMININ N-TERMINAL (DOMAIN VI).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (C-TERMINAL).
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 11.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 16.
LAMININ EGF-LIKE 17.
DOMAIN I AND I.
LAMININ G-LIKE 17.
LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
       SIMILARITY: Contains 2 laminin IV domains. SIMILARITY: Contains 5 laminin G-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 129:257-262(1993)'
-!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
-!- DOMAIN: CONTAINS 29 REPEATS OF THE CXXC MOTIF.
-!- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
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"Two genes encoding homologous 70-kDa surface proteins are present
within individual trophozoites of the binucleate protozoan parasite
Giardia intestinalis.";
                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=ATCC 30957 / WB;

MEDLINE=90280395; PubMed=2352929;

Gillin F.D., Hagblom P., Harwood J., Aley S.B., Reiner D.S.,

McCaffery M., So M., Guiney D.G.;

"Isolation and expression of the gene for a major surface protein of archia lamblia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL) (POTENTIAL)
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N-LINKED (GLCNAC. .) (POTENTIAL
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A -> S (IN STRAIN ADELAIDE-1).
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                                                                                                     Giardia lamblia (Giardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBI_TaxID=5741;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Major surface-labeled trophozoite antigen 417 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTIGEN 417.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990)
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InterPro; IPR005127; Giardia VSP.
InterPro; IPR009030; Grow fac_recep.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93314970; PubMed=8325510;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 480-620 FROM N.A.
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EMBL; M97488; AAA02581.1; -.
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58; Conservative
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SMART; SM00181; EGF; 1.
SMART; SM00261; FU; 3.
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PIR; PC1294; PC1294.
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MEDLINE=94124633; PubMed=8294519;
Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
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chromosomal assignment, and expression of the M and A chain in human
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Neurology 57:1319-1322(2001).
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He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
Estournet-Mathiaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                      P24043; O14736; O93022;
01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
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Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E "Merosin, a tissue-specific basement membrane protein, is laminin-like protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                   475 -TCGLTIDGASYCSECATTTEYPQNGVCAPKASRATPTCNDSPIQNG
                                                                                                                                    137 INCSL--DGRSVLK--TGTTE--KDVVCGPPVVSFSPSTTISVTPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97066955; PubMed=8910357;
Zhang X., Vuolteenaho R., Tryggvason K.;
"Structure of the human laminin alpha2-chain affected in congenital muscular dystrophy.";
J. Biol. Chem. 271:27664-27669(1996).
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Marzluf G.A., Amato A.A., Mendell J.R.;
Hum. Mutat. 13:340-340(1999).
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MEDLINE=22439669; PubMed=12552556;
104 DCRPGQELTKQGCKTCSLGTFND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol. 124:381-394(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAMA2 OR LAMM
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Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M., Anglain C., Hoffman E.P., Pegoraro E.; Anglain C., Hoffman E.P., Pegoraro E.; Park J., Tygon M., Finkel R., Garcia C., Anglain C., Hoffman E.P., Pegoraro E.; Partial laminin alpha-Z (LAMA2) deficiency."; partial laminin colliscues during embryonic development by interacting of there extracellular matrix components.

1. FUNCTION: Binding to cells via a high affinity receptor, laminin of cells into tissues during embryonic development by interacting with other extracellular alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comparising one long and three short arms with globules at each end. The alpha-Z chain is a subunit of laminin-2 (merosin) and laminin-4 (S-merosin).

1. SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).

2. SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).

3. TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve, sxin, testis, meninges, chorid plexus, and some other regions of the brain, not in liver, thymus and bone.

3. TISSUE DEFICIENT TO and Gameins I and in are thought to interact with other laminin chains to form a coiled coil structure.

3. DOMAIN: The alpha-helical domains I and white matter hypodensity on MRI.

4. DISBABS: Defects in LAMA2 are the cause of merosin-deficient congenital muscular dystrophy type 1A (Molecular Process), hyporeflexia, and wind walter hypodensity on MRI.

5. SIMILARITY: Contains I mainin Wellen and commined to main the domains.

5. SIMILARITY: Contains I mainin Meromine.
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EMBL; Z26653; CAA81394.1; -
EMBL; U66736; AAB18388.1; -
EMBL; U66734; AAB18388.1; JOINED.
EMBL; U66735; AAB18388.1; JOINED.
EMBL; U66735; AAB18388.1; JOINED.
EMBL; U66736; AAB18388.1; JOINED.
EMBL; U66737; AAB18388.1; JOINED.
EMBL; U66739; AAB18388.1; JOINED.
EMBL; U66740; AAB18388.1; JOINED.
EMBL; U66741; AAB18388.1; JOINED.
EMBL; U66745; AAB18388.1; JOINED.
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EMBL; U66745; AAB18388.1; JOINED.
EMBL; U66746; AAB18388.1; JOINED.
EMBL; U66746; AAB18388.1; JOINED.
EMBL; U66747; AAB18388.1; JOINED.
EMBL; U66749; AAB18388.1; JOINED.
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GO, GO:0005199; F:structural molecule activity; TAS.
GO; GO:0005199; F:structural molecule activity; TAS.
GO; GO:0005199; F:structural molecule activity; TAS.
GO; GO:0007517; P:muscle development; TAS.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR008031; Laminin_EGF.
DR InterPro; IPR008031; Laminin_EGF.
DR InterPro; IPR00821; Laminin_EGF.
DR InterPro; IPR00821; Laminin_EGF.
DR Ffam; PF00052; laminin_EGF. 14.
DR Ffam; PF00052; laminin_G; 5.
DR Pfam; PF00052; laminin_G; 5.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00052; laminin_B; 1.
DR PR0011; EGF_Lam; 15.
DR RART; SM00136; Lamin; 15.
DR SWART; SM00136; Lamin; 16.
DR ROSITE; PS01248; LAMININ_TYPE EGF; 14.
DR PROSITE; PS01248; LAMININ_TYPE EGF; 14.
DR PROSITE; PS01248; LAMININ_TYPE EXTRAcellular matrix; Coiled coil; KW laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism; KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism; KW Jisease mutation.
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EMBL; U66763; AAB18388.1; JOINED.
EMBL; U66765; AAB18388.1; JOINED.
EMBL; U66766; AAB18388.1; JOINED.
EMBL; U66769; AAB18388.1; JOINED.
EMBL; U66770; AAB18388.1; JOINED.
EMBL; U66771; AAB18388.1; JOINED.
EMBL; U66772; AAB18388.1; JOINED.
EMBL; U66773; AAB18388.1; JOINED.
EMBL; U66774; AAB18388.1; JOINED.
EMBL; U66775; AAB18388.1; JOINED.
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EMBL; U66778; AAB18388.1; JOINED.
EMBL; U66778; AAB18388.1; JOINED.
EMBL; U66786; AAB18388.1; JOINED.
EMBL; U66789; AAB18388.1; JOINED.
EMBL; U66799; MAHUMH.
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                                                     ----CEKD----C 105
                                                                                VCHS-QTGQCECRANVQGQRCDKCKAGTFGLQSARGCVPCNCNSFGSKSFDCEESGQCWC 987
                                                                                                                          RPGQBLTKQGCKTCSLGTFNDQNG------TGVCRPWTNCSLDGRSVLKTGTT-EK 154
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RA TISSUE=Brain,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

BA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rodergren E.J., Norfigues S., Sanchez A.,

Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=89096903; PubMed=2850481;
Sehgal A., Patil N., Chao M.;
"A constitutive promoter directs expression of the nerve growth factor receptor gene.";
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MEDLINE=99445585; PubMed=10514511;
Ye X., Mehlen P., Rabizadeh S., VanArsdale T., Zhang H., Shin H.,
Wang J.J., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(G75 CD) (Low affinity neurotrophin receptor p75NTR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87051725; Pubmed=3022937;
Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer
Bothwell M., Chao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression and structure of the human NGF receptor."; Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                            427 AA.
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Mol. Cell. Biol. 8:3160-3167(1988).
                                          FCSSTHNAECEC---IEGFHC---
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01-AUG-1988 (Rel. 08, Last seq.
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                     1041 CSKCAPNTWGHSITT 1055
                                                                                                                                                                                                          DVVCGPPVVSFSPST 169
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGFR OR TNFRSF16
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                                                                                                                                                                                                                                                                                                                                                       TR16 HUMAN
P08138;
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TR16_HUMAN
ID TR16_HUMAN
ID TR16_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"TRAF family proteins interact with the common neurotrophin receptor and modulate apoptosis induction."; J. Biol. Chem. 274:30202-30208(1999).
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20012928; Pubmed=10544233;
Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
Reed J.C., Bredesen D.E., Sato T.A.;
"Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
FDTS (NTR) and their effect on NF-kappaB activation.";
FEBS Lett. 460:191-198(1999).
-!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3
and NT-4. Can mediate cell survival as well as cell death of
neural cells.
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REMBL; M14764; AABS95941.1; -.

REMBL; M2050309; AAH50309.1; -.

REMBL; M21621; AAA36363.1; -.

REMBL; M21621; AAA36363.1; -.

REMBL; M205174; 1NGR.

RENDS; P07174; 1NGR.

RENDS; P0707000; TNFR C6; 4.

RENDS; P0707000; TNFR; 3.

RENDS; P0707000; TNFR; 3.

RENDS; P070700; TNFR; 3.

RENDS; P070700; TNFR; 3.

RENDS; P070700; TNFR; 3.

RECEPTOR; APOPTOSIS; Neurogenesis; Transmembrane; Glycoprotein; P0707000; TNFR; 3.

RECEPTOR; APOPTOSIS; Neurogenesis; Transmembrane; Glycoprotein; P0707000; TNFR; 3.

RECEPTOR; ADOPTOSIS; Neurogenesis; Transmembrane; Glycoprotein; P0707000; TNFR; 3.

RECEPTOR; ADOPTOSIS; Neurogenesis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor. Interacts with TRAF2, TRAF4, TRAF6 and PTPN13.
                                                                                                                                                                            MEDLINE=99115593; PubMed=9915784;
Khursigara G., Orlinick J.R., Chao M.V.;
"Association of the p75 neurotrophin receptor with TRAF6.";
J. Biol. Chem. 274:2597-2600(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUPERFAMILY MEMBER 16.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PTM: N- and O-glycosylated.
-!- PTM: Phosphorylated on serine residues.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
-!- SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH.
SER/THR-RICH.
BY SIMILARITY
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH PTPN13.
                                                                                                                                           INTERACTION WITH TRAFE,
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T10D HUMAN
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                                                                                                                                                                                                                                                          54 S-IGGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCE--KDCRPGQE 110
                                                                                                                                                                                                                                                                            3 DVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRCAYGYY-QDETTGRCEACRVCEAGSG 133
                                                                                                                                                                                                                                                                                                              111 LT----KQG--CKTCSLGTFNDQ-NGTGVCRPWINCSLDGRSVLKTGTTEKDVVC---- 158
                                                                                                                                                                                                                                                                                                                              134 LVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVCE-DTERQLRECTRWADAECEEIP 192
                                                                                                                                                                                                                                                                                                                                                                  159 -----GPPVVSFS--PSTTISVTPEGGPG-------GHSLQVLT---- 188
                                                                                                                                                                                                                                                                                                                                                                                            193 GRWITRSTPPEGSDSTAPSTO---EPEAPPEODLIASTVAGVVTTVMGSSOPVVTRGTTD 249
                                                                                                                                                                                                      53
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                                                                                                                                                                                                                              15 LLLLLLLGVSLGGAKEACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFS
                                                                                                                                                                                                     10 VIVLLIVGCEKVGAVQ-----NSCDNCQPGTF----CRKYNPVCKSCPPS-TFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alternative polyadenylation sites.";

alternative polyadenylation sites.";

Gene 133:307-308(1993).

-! FUNCTION: INTEGRIN ALPHA-V/BETA-S IS A RECEPTOR FOR FIBRONECTIN.

IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.

-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5

ASSOCIATES WITH ALPHA-V.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- PTM: The cysteine residues are involved in intrachain disulfide
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

MW; B09FA143FB3D625B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papio cynocephalus (Yellow baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=9404040831; PubMed=8224922;
Shoji M., Hayzer D.J., Kim T.M., Runge M.S., Hanson S.R.;
"Human and baboon integrin beta 5 subunit-encoding mRNAs have
                                                                                                                                                 Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the integrin beta chain family.
                                                                                                                                                                             97; Indels
                                                                                                                                                9.5%; Score 135; DB 1;
25.2%; Pred. No. 0.00054;
live 26; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    250 NLIPVYCSILAAVVVGLV 267
                                                                                                                        45183 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ntegrin beta-5 (Fragment).
                                                                                                                                                              Local Similarity 25.2
Les 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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427 AA;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 10D precursor (Decoy receptor 2) (DCR2) (TNF-related apoptosis-inducing ligand receptor 4)
(TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCDNCQ--PGTFCRKYNPVCK----SCP--PSTFSSIGGQPNCNICRVCAGYFRFKKFCS
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                                                                                      InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR00169; Integrin B.
InterPro; IPR002035; VWF A.
InterPro; IPR002035; VWF A.
InterPro; IPR00181; INTEGRIN B; 1.
PRINTS; PR01186; INTEGRIN B; 1.
SWART; SM00181; EGF; 1.
SWART; SM00187; INB; 1.
SWART; SM00327; VWA; 1.
R SWART; PS00224; INB; 1.
R PROSITE; PS00225; EGF 1; UNKNOWN 2.
R PROSITE; PS01186; EGF 2; UNKNOWN 2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
R Repeat; Extracellular matrix; Cytoskeleton.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 TISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI--RKKF 218
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(POTENTIAL).
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BAC33A159CBE1596 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
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or send an email to license@isb-sib.ch).
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INFRSF10D OR DCR2 OR TRAILR4 OR TRUNDD.
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                                               EMBL; L12231; AAA16866.1; -.
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510
561
655 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;

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Matches
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RT SISURE-Prostate;

RA MIDLINE-22388257; PubMed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H.M. Moore T., Max B. Mong J., Haish F.,

Datchenko L., Marushan K., Farmer A.A., Rubin G.M., Hong L.

Rablecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahey J., Touchman J.W., Green E.D., Dickson M.C.,

Rahey J., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.L., Shalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.L., Shalska U., Smailus D.E.,

C. Grimwood J., Schmutz J., Myers R.M.,

Butterfield X.S.N., Krzywinski M.L., Stablska U., Smailus D.E.,

C. Grimwood J., Schmutz J., Myers R.M.,

Butterfield X.S.N., Krzywinski M.L., Stablska U., Smailus D.E.,

C. Grimwood J., Schmutz J., Myers R.M.,

Butterfield X.S.N., Krzywinski M.L., Stablska U., Smailus D.E.,

C. FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a poptosis but protects against TRAIL-mediated apoptosis. Reports are contradictory with regards to its ability to induce the NF-

Ref. 2 it can induce the NF-kappa-B pathway).

C. FUNCTION: Receptor for the cytotoxic ligand transpace of inducing a poptosis but protects against TRAIL-mediated apoptosis. Reports are contradictory with regards to its ability to induce the NF-

Ref. 2 it can induce the NF-kappa-B pathway).

C. FUNCTION: Receptor for the cytotoxic ligand transpace before a contradictory with regards to its ability to induce the NF-

C. Subber 
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                                                                                                  TISSUE=Fetal lung;
MEDLINE=98044290; PubMed=9382840;
Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,
Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,
Ashkenazi A.;
"A novel receptor for Apo2L/TRAIL contains a truncated death domain.";
Curr. Biol. 7:1003-1006(1997).
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS SER-35 AND LEU-310. TISSUE=Foreskin fibroblast, and Peripheral blood lymphocytes; MEDLINE=98090091; Pubmed=9430226; Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=98196860; PubMed=9537512;
Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;
"TRUNDD, a new member of the TRAIL receptor family that antagonizes
                                                                                                                                                                                                                                                                                                                                                                                                                          "The novel receptor TRAIL-R4 induces NF-kappaB and protects against TRAIL-mediated apoptosis, yet retains an incomplete death domain."; Immunity 7:813-820(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intestine, ovary, prostate, thymus, spleen, pancreas, kidney, lung, placenta and heart.
                                                                           FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
-!- SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRAIL signalling.";
FEBS Lett. 424:41-45(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 EECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQINKSSCTTTRDTVCQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 CIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPW-TNCSLDGRS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 VLKTG--TTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 DNCQPGTFCRKYNPVCKSCPPSTFSSIGGO--PNCNICRVCAGYFRFKKFCSSTHNAECE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 ITLLFSVLKWI-----RKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEGGGGGYE 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77; Gaps
                                                                                                                                                                                                                                                        PinterPro; If, 197001368; TNFR_c6.
Pfam; PF00020; TNFR; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;
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DEATH (TRUNCATED).

POLY-VAL.

POLY-GLY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUPERFAMILY MEMBER 10D. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_011418.
77A93577CAAF2632 CRC64;
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/FTId=VAR_011417.
S -> L (in TRAIL-R4-B)
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ID TIBS HUMAN STANDARD; PRT; 799 AA.

AC P18084;
DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

BE Integrin beta-5 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS 2
                            AF029761; AAD03477.1; -.; AF021232; AAC32765.1; -.; AF021233; AAC32766.1; -.; AF023849; AAC52053.1; -.; BC052270; AAH52270.1; -.
                                                                                                     EMBL; AFULL
EMBL; BC052270; ALLL
HSSP; 014763; 1D4V.
"enew; HGNC:11907; TNFRSF10D.
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386
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us-10-067-122b-2.rsp

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Query Match
Best Local Similarity 27.7%; Pred. No. 0.0012;
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps
DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR00169; Integrin_B.

DR InterPro; IPR00169; Integrin_Beta_C.

DR InterPro; IPR003035; VWF_A.

DR InterPro; IPR00362; integrin_B; 1.

DR PRINTS; PR01186; INTEGRINE.

DR SWART; SM00187; INB; 1.

DR SWART; SM00423; PSI; 1.

DR SWART; SM00327; VWA; 1.

DR PROSITE; PS0022; EGF_1; UNKNOWN_2.

DR PROSITE; PS01186; EGF_2; UNKNOWN_2.

DR PROSITE; PS01186; EGF_2; UNKNOWN_2.

RW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein; Transmembrane; I SIGNAL.

THE STANDAL I 23 DOMENTIAL.
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INTEGRIN BETA-5.
EXTRACELLULAR (POTENTIAL)
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VWFA-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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799 AA;
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SEQUENCE FROM N.A.

REQUENCE FROM N.A.

RETUSSUE-Kidney,

A Itschul S.F., Zeeberg B., Grouse L.H., Derge J.G., Bhat N. K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Scapleton M., Soares M.B., Bonaldo M.F., Carvinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,

Rachards S., Worley K.C., Hale S., Garzia A.M., Gay L.J., Hulyk S.W.,

RACHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RACHARGS S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rachards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

RACHARGS S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

RACHARGS S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

RACHARGS S., McThamon J.W., Green E.D., Dickson M.C.,

RA Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

RACHING M., Schein J.E., Jones S.J.M., Marra M.A.,

Romeration and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.

IT SECONITES WITH ALPHA-V.

C. -- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5

C. -- SUBUNIT: HETERODIMER OF AN ALPHA AND C. SUBURIT.

SUBUNIT: HETERODIMER OF WILLE INTEGRIN PARA CORPITOR.

C. -- SUBUNIT: HETERODIMER OF WILLE INTEGRIN PARA CORPITOR.

C. -- SUBUNIT: HETERODIMER OF WILLE INTEGRIN PARA CORPITOR.

C. -- SUBUNIT: HETERODIMER OF WILLE INTEGRIN PARA 
                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Thymic epithelium;
MEDLINE=90228356; PubMed=2328726;
Ramaswamy H., Hemler M.E.;
"Cloning, primary structure and properties of a novel human integrin
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90319111; PubMed=2371275;
Suzuki S., Huang Z.S., Tanihara H.;
"Cloning of an integrin beta subunit exhibiting high homology with integrin beta 3 subunit.";
Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).
                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[11]
                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
MEDLINE=91009141; PubMed=2211615;
MCLean J.W., Vestal D.J., Cheresh D.A., Bodary S.C.;
"CDNA sequence of the human integrin beta 5 subunit.";
J. Biol. Chem. 265:17126-17131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X53002; CAA37188.1; -.
EMBL; M35011; AAA52707.1; -.
EMBL; J05633; AAA59183.1; -.
EMBL; BC006541; AAH06541.1; -.
PIR; A38308; A38308.
HSSP; P05106; 1JV2.
Genew; HGNC:6160; ITGBS.
MIM; 147561; -.
                                                                                                                                                                                                                                beta subunit.";
EMBO J. 9:1561-1568(1990).
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14; 78 27 SCDNCQ--PGTFCRKYNPVCK----SCP--PSTFSSIGGQPNCNICRVCAGYFRFKKFCS

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                                                                                                121
                                                                                                                                                                 646
                                                                                                                                                                                                                                  169
                                                                                                                                                                                                                                                                                     647 LHSGKPDNQTCHSLCRDEVITWVDTIVKDDQEAVLCFYKTAKDCVMMFTYVELPSGKSNL 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein
                                                                                           STHNAECE-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKQGCKTCSL
                                                                                                                                                         STDISTCRGRDGQICSERGHCLCGQCQCTEPGAFGEMCEKCPTC-PDACSTKRDCVECLL
                                                                                                                                                                                                                         ---GTFNDQNGTGVCR----PWTNCSL--DGRSVLKTGTTEKDVVCGPPVV---SFSPST
STRAIN=Brighton red;
MEDLINE=94378510; PubMed=8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";
virology 204:343-356(1994).
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=GRI-90 / Grishak;
MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
"The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                     TISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI--RKKF 218
                                                                                                                                                                                                                                                                                                                                                                                                                              754
                                                                                                                                                                                                                                                                                                                                                                                                HSSF; O14,03; 1003.
InterPro; IPR001368; TNFR_c6.
SMEM; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR, 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Glycoprotein; Repeat; Signal.
SIGNAL
20 351 SOLUBLE TNF RECEPTOR'II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRMB_COWPX STANDARD; GOT3559; P87602; 28-FEB-2003 (Rel. 41, Last sequin-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X94355; CAA64087.2; -.
EMBL; X94355; CAD90756.1; -.
HSSP; O14763; 1D0G.
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NCBI_TaxID=10243;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases:

(aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).

-!- SUBUNIT: Binds DAXX and RIPKI (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        44 CLSCPPGTYASRLCDSKTNTNTQCTPCGSGTPTSRNNHLPACLSCNGRCDSNQVETRSCN 103
                                                                                                                                                                                                                                                                                                                                                                               79 STHNAECECIEGFHCL---GPQCTRC--EKDCRPGQEL---TKQG---CKTCSLGTFNDQ 127
                                                                                                                                                                                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                          CDNCQPGTFCRKY-----NPVCKSCPPSTFSSIGG-PNCNICR-VCAGYFRFKKFCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D., "Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL
receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                  1 9.3%; Score 133.5; DB 1; Length 351; Similarity 29.5%; Pred. No. 0.00059; B; Conservative 14; Mismatches 56; Indels 21.
                                               BY SIMILARITY.
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15-JUL-1999 (Rel. 38, Last seq
10-OCT-2003 (Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38,
10-OCT-2003 (Rel. 42,
Tumor necrosis factor
                                                                                                                                          103
191
250
351 AA;
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SEQUENCE FROM N.A.
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REPEAT
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60 -NCNICRVCAGY--FRFKKFCSSTHWAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                      97 SKCRRCRVCDGEHGLEVEKNCTRTQNTKCRCKPNFFCHTSQCEHCNP------C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor (Lowaffinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(p75 ICD) (Low affinity neurotrophin receptor p75NTR).
NGFR OR TNFRSF16.
Rattus norvegicus (Rat).
EMBL; AJ001202; CAA04596.1; -...

R HSSP; P25445; 1DDF.

RICEPTO; IPR000488; Death.

InterPro; IPR001368; THRE_C6.

InterPro; IPR001368; THRE_C6.

R InterPro; IPR001368; THRE_C6.

R Ffam; PF00531; death; 1.

R Ffam; PF00531; death; 1.

R FRINTS; PR01680; FASRECEPTOR.

R SMART; SM00005; DEATH; 1.

R RANAT; SM00008; THRE, 3.

R RANAT; SM00508; THRE_NGFR_1; 2.

R RROSITE; PS50017; DEATH DOMAIN; 1.

R Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

T SIGNAL

T CHAIN 17 332 THMOR NET SMETTOR
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                  DEATH.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

W; SB8B03682756BF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                           TUMOR NECESTS FACTOR RECEPTOR SUPERFAMILY MEMBER 6.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                              9.3%; Score 133; DB 1; Length 332; 26.1%; Pred. No. 0.00061; tive 10; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 KTCSLGTFNDQNGTGVCRPWTN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87115859; PubMed=3027580;
                                                                                                                                                                                                                                                                                                                             37592 MW;
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3322
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11255
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TR16 RAT
ID TR16 DAT
DT 01-AP
DT 10-OC
DE TUMOCT
DE AFIN
DE (P75
GN NGFR
OC BUKAT
OC BUKAT
OC MAMMA
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Agadee W.J., Misko T.P., Bau C.; Herrenherg L.A., Shooter E.W.; Grant Errenfor and objectular clouding of the rat neave growth factor and water of the control of the rat neave growth factor and the control of the rat neave growth factor and the control of the rat neave growth factor receptor; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the rat neave growth factor receptor promoter.; and relations of the passage of the rat neave growth factor receptor promoter.; and relations of the passage of the rat neave growth factor receptor promoter.; and relations of the passage of the rat neaver growth factor receptor promoter. The promoter of the death domain of the pis matrices with pristre. Brown of the passage of the relations of the passage of the rat neaver growth factor receptor factor of the relations of the passage of the rat neaver growth factor companies. The relations of the passage of the rat neaver growth factor relations of the passage of the rat neaver growth growth of the passage of the rate of the relations of the passage of the rate of the relations of the passage of the rate of the relations of the passage of the rate of the relations of the passage of the rate of the relations of the passage of the relations of the passage of the rate of the relations of the passage of the relations of the passage of the rate of the relations of the passage of the passage of the passage of the passage of the passage of the passage of the pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 GLVFSCQDXQNTV---CEECPEGTYSDEANHVDPCLPCTVCE-DTERQLRECTPWADAEC 189
                                                                                                                                                                                                                                                                                                                                                                                                      54 S-IGGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGF-----HCLGPQCTRCEK-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 ---- DCRPGQELTKQGCKTCSLGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 DVVSATEPCKPCTECLGLQSMSAPCVEADDAVCRCAYGYYQDEETGHC--EACSVCEVGS 133
                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                           16 LLLLLILGVSSGGAKETCSTGLYTHSGECCKACNLGGGVAQPCGANQTVCEPCLDNVTFS
                                                                                                                                                                                                                                                                                                      10 VIVLLIVGCEKVGAVQ------NSCDNCQPGTF----CRKYNPVCKSCPPS-TFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Camelpox virus (strain CMS), and Camelpox virus (strain M-96). Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

W, B2E152D94D3827F8 CRC64;
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PubMed=11907336;
Gubser C., Smith G.L.;
"The sequence of camelpox virus shows it is most closely related variola virus, the cause of smallpox.";
J. Gen. Virol. 83:855-872(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210)
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-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contrithe modification of TNF-mediated antiviral processes (By
                                                                                                                                                                                                      ; Score 133; DB 1; Length 425;
; Pred. No. 0.00078;
20; Mismatches 88; Indels
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SUBCELLULAR LOCATION: Secreted (By similarity).
SIMILARITY: Contains 2 TNFR-Cys repeats.
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NCBI_TaxID=203172, 203173;
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1es 51; Conservative
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  DISULFID
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CRMB_CAMPS
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104 HNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGVSGHTSAGDVICSPCGLGTYSRTVS 163
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TUFR-CYS 1.
TUFR-CYS 2.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                          Repeat; Signal
EMBL; AY009089; AAG37456.1; -.
EMBL; AY009089; AAG37718.1; -.
EMBL; AF438165; AAL73920.1; -.
EMBL; AF438165; AAL73917.1; -.
InterPro; IPR001368; TNFR_c6.
Ffam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR_c6; 2.
PROSITE; PS500652; TNFR_NGFR_1; 2.
PROSITE; PS500652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Glycoprotein; Repeat; SigsIGNAL
1 19 SOLUBL
CHAIN
20 349 SOLUBL
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Q94j12 cowpox viru Q7zzy5 gallus gall Q8jfv6 brachydanio Q8vc17 mus musculu Q8vc17 mus musculu Q8uyl3 vaccinia vi Q9ujb4 vaccinia vi Q9ujb4 vaccinia vi Q9ujb4 vaccinia vi Q9uys6 oncorhynchu Q8uys7 cowpox viru Q9pus0 salvelinus Q9pus0 cowpox viru Q9prg7 cowpox viru Q9prg7 cowpox viru Q9prg7 cowpox viru Q9prg0 ovis aries Q7t2h3 oncorhynchu Q8wmq2 ovis aries Q7t2h3 oncorhynchu Q8ymq2 ovis aries Q7t2h3 oncorhynchu Q8ymq2 ovis aries Q7t2h3 oncorhynchu Q8ymq2 cowpox viru Q8bru6 mus musculu Q9dfv0 brachydanio Q8jfu6 brachydanio Q8jfu6 brachydanio Q8jfu6 prachydanio lam
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canis famil
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to tumor necrosis factor receptor superfamily, member 9.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.0%; Pred. No. 1e-111;
Matches 210; Conservative 0; Mismatches 1; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028507; AAH28507.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS01186; EGF 2; 1.
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Q92762
Q91ZM6
Q80WY6
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Q7T2H3
O57484
Q9JKE0
Q8JFU6
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Q9DFV0
O57111
O72761
                  Q9DJL2
Q7ZZYS
Q8JFV6
Q8VC17
Q8UYL3
Q911R5
Q9WJB4
O72735
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TISSUE=Uterus;
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QB00k7 paralichthy
QB00i0 gallus gall
QBc4k3 mus musculu
QBddd2 gallus gall
QB6yk5 homo sapien
QB05b0 gallus gall
QBk2x6 mus musculu
QB2327 mus musculu
QB1x6 homo sapien
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1 MGNNCYNVVVIVLLLVGCEK......DACSCRCPQEEEGGGGGYEL 256
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q80WM9
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NCBL_TaxID=9031;
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01-JUN-2003
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                                                                                      240
                                      LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPA 180
                                                                                                                              -----FKKTTGAAQEEDACS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΨĮ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 RC--EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 İNSTDITCSSQVVYYVVS------ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQE-CSSWKDTVCRC1PGYFCENQDGSHCS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NNCYNVVVIVLLLVGCEKVGAV-----QNSCDNCQPG----TFCRKY-NPVCKS 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPPSTFSS-IGGOPNCNICRVC---AGYFRFKKFCSSTHNAECECIEGFHCL---GPQCT 99
                                                                            181 GHSLQVLTLFLALTSALLLALIPITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTBKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 TCLOHTTCPPGORVEKRGTHDODTVCADCLTGTFSLGGTQEECLPWTNCSAFQQEV-RRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6; TISSUE=Thymus;
Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
Light regulation in a murine model of ovarian carcinoma.";
Light regulation in a murine model of ovarian carcinoma.";
Lushi Av264405; DA089081.1;
RMBL; Av264405; AA089081.1;
RGO; GO:0006988; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
RGO; GO:0007165; P:signal transduction; IEA.
RILEPPO; IPR008063; Fas receptor.
RILEPPO; IPR001368; TNFR.c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%; Score 225; DB 11; Length 275; 26.2%; Pred. No. 7.7e-15; ive 31; Mismatches 111; Indels 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4A7EAD8EFC0521D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RR---HLHTSSVAKELEPFÖEQQENTIRFPVTEVG 264
                                                                                                                                                                                                                                                                                                                            275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential
                                                                                                                                                                                                                                                                                                                            PRT;
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PROSITE; PS50050; TNFR NGFR 2; 3.
Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 P
                                                                                                                                                                    CRCPOEEEGGGGGYEL 256
                                                                                                                                                                                                          196 CRCPQEEEGGGGYEL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01680; FASRECEPTOR. M00208; INFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c6; 4
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                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                         181
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SMART; S
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Park C., Kurobe T., Hirono I., Aoki T.;

"Cloning and characterization of cDNAs for two distinct tumor necrosis

"Cloning and characterization of cDNAs for two distinct tumor necrosis
factor receptor superfamily genes from Japanese flounder Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKFCSSTHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 TGCVCKPGMYCIMDFDNPYCAECRNYSQCRAGYGVSLPGKANSDVKCELCPDGMFSNTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AECECIEGFHCL----GPQCTRCE--KDCRPGQELIKQG------CKTCSLGTF-NDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes; Pleuronectoidei, Paralichthyidae, Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 15.1%; Score 215.5; DB 13; Length 483; Local Similarity 25.6%; Pred. No. 1.3e-13; les 70; Conservative 31; Mismatches 93; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         olivaceus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 AA; 52227 MW; EE55874A8C7F2085 CRC64;
                                                                          , Last sequence update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 TLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB080947; BAC65226.1; -. GO; GO: 0004872; F:receptor activity; IEA. InterPro; IPR001368; TNFR C6. Pfam; PF00020; TNFR C6; 3.
                                                    Created)
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                                                                                                                                                                               Paralichthys olivaceus (Flounder)
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SMART; SM00208; TNFR, 4.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 3.
                                                                                                                          necrosis factor receptor-2.
                                         (TrEMBLrel. 24, I
(TrEMBLrel. 24, I
(TrEMBLrel. 25, I
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- CKTCSLGTF-NDONGTGVCRPWTNCSLDGRSVLKTGTTE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 SIGGOPNC-----NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPQCTRCE 102
                                                                                                                                                                                                                                                                                 103 K-DCRPGOELTKOG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154
                                                                                                                                                                                                                                                                                                                                     22 SVVBEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VIVILLYGCEKVGAVQN-----SCDNCQPG----TFCR-KYNPVCKSCPPSTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CD40-homologue.
INFSF5.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             155 DVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI
                                                                         41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
EMBL; AJ293700; CAC20218.1; -.
HSSP; Q92956; 1JMA.
     Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 199; DB 13; Length 276; 24.6%; Pred. No. 3.6e-12; cive 40; Mismatches 96; Indels 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R GO; GO:0016020; C:mucleus; IEA.

R GO; GO:0016020; C:mucleus; IEA.

R GO; GO:0004888; F:transmembrane receptor activity; IEA.

R GO; GO:0006915; P:apoptosis; IEA.

R GO; GO:0006915; P:apoptosis; IEA.

R GO; GO:0006915; P:apoptosis; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR001006; Myb_DNA_binding.

R InterPro; IPR001005; Myb_DNA_binding.

R Pfam; PF00020; TNFR_C6; 3.

R PRINTS; PR001680; FASRECEPTOR.

R PROSITE; PS00037; MYB_1; 1.

R PROSITE; PS00652; TNFR_NGFR_1; 1.

R PROSITE; PS00652; TNFR_NGFR_1; 1.

R PROSITE; PS00652; TNFR_NGFR_1; 1.
                                                    84; Indels
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Last annotation update)
  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 RKKFPHIFKOPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 14.3%; Score 203.5; DB 1
1 Similarity 29.8%; Pred. No. 1.1e-12;
64; Conservative 26; Mismatches 84
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Best Local Similarity 24.6'
Matches 73; Conservative
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              Query Match
                                                    Best Local
Matches 6
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

X MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

I analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

RMD, MGI:894675; Thfref18.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR.C6.

RMART; SM00208; TNFR, 2.

RMART; SM00208; TNFR, 2.

SEQUENCE 250 AA; 27814 MW; 6963E94F414C16B4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 CYQCPSGYAKKKSCPMDPDEDCMRCGPEQYLNQSPKPRCDACVLCTKEFDLVEKAPCSFN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 HNAECECIEGFHC---LGPQCTRCEKD--CRPGQELTKQG-----CKTCSLGTFNDQ- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CDNCQPGTFCRKYNPV----CKSCPPSTFSSIGGQPNCNICRVCAGYFRF--KKFCSST 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SPSTTISV-----TPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSF---------
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCEL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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Best Local Similarity 24.4%; Pred. No. 1.5e-12;
Matches 69; Conservative 36; Mismatches 116; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgess S.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 21 Potential.
22 467 CD30 protein.
467 AA; 51350 MW; F9AD4F77DEEC8588 CRC64;
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Thesis (1998), Bristol University, U.K.
EMBL; AJZ76964; CAC79223.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR c6.
Pfam; PF00020; TNFR c6; 3.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR NGFR 1; 2.
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Q8C4K3
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AC QBK2X6;
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EPCKQGFGFVAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCEEKGLVVKVKGTNT 182
                                                       KDVVCGPPVVSFSPSTIISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKW 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                 70 Y--FRFKKFCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPG------QELTKQGCKT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 NLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEP 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                  -----PFKKTTGAAQ---EEDACSCRCPQEEE 248
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SEQUENCE FROM N.A.

He X., Xu L., Zeng Y.;
He X., Xu L., Zeng Y.;
He X., Xu L., Zeng Y.;
He X., Xu L., Zeng Y.;
He X., Xu L., Zeng Y.;
He X., Xu L., Zeng Y.;
He EMBL, Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

Rebels, AY225405; AA043990.1;
Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Replander Rep
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-2003 (TrEMBLrel. 24, Created)
N-2003 (TrEMBLrel. 24, Last sequence update)
T-2003 (TrEMBLrel. 25, Last annotation update)
necrosis factor receptor superfamily member 5 (Fragment)
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PROSITE; PS00215; MITÖCH CARRIER; 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 4.
                                                                                                                183 SDVIC----ESSRRSSLSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; TNFR c6; 4. PRINTS; PR01680; FASRECEPTOR.
                                                                                                                                                                               214 IRKKFPHIFKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00208; INFR:
                                                                                                                                                                                                                                                                                                                                                                                                                     Q86YK5;
01-JUN-2003
01-JUN-2003
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NON TER
SEQUENCE
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Q86YK5
ID Q86Y
AC Q86Y
DT O1-J
DT O1-J
DT O1-J
DT O1-J
DT O1-G
DE EUKa
OC BUKa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                 Incali.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSSTHNAECECIEGFHCLGPQCTRC----EKDCRPGQELTKQG------CKTCSLGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 SDEESYDTSCIPHTVC----KSVAVAGNNVNDTVCHDSVATALPHTAVNFLPSQSSTTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 NDQNGTGV-CRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 LQVLT-------LFLALTSALLLALIFITL---LFSVLK-------WIRKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=White leghorn. H-B15; TISSUE=Spleen;
Sayed A., Horuchi H., Furusawa S., Matsuda H.;
Sayed A., Horuchi H., Furusawa S., Matsuda H.;
Molecular cloning and characterization of chicken Tumor necrosis factor receptor Tassociated factor-I (TNFR-II) and Tumor necrosis factor receptor associated factor-5 (TRAF-5) genes.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB101004; BAC55966.1; -.

RO; GO:0006915; P:membrane; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:immune response; IEA.

GO; GO:000165; P:signal transduction; IEA.

RO;  GO:0006955; TNFR C6; 3.

ROSITE; PS00652; TNFR NGFR 1; 2.

ROSITE; PS00652; TNFR NGFR 1; 2.

R PROSITE; PS00652; TNFR NGFR 2; 3.

R PACELLE 1: PS00652; TNFR NGFR 2; 3.

R PACELLE 2: RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sayde A.A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 AA; 50141 MW; 8B00A93305414782 CRC64;
                                                           (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.1%; Score 187; DB 13; 24.1%; Pred. No. 1.1e-10; ive 36; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 PHIFKOPFKKTTGAAQEEDACSCRCPQEEE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPTEKOCDKKVRNAGSONSSSS---EQEEO 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-White leghorn H-B15; TISSUE-Spleen; Sayde A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                Tumor necrosis factor receptor-II.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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159 -----GPPVVSFS-----PSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 VNYQACKPCTQC-----NRRSGSEPQQECT----HTRDTVCR-----CRPGTQPLNGY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LLILGLILGABPRPDCVGDTYPGGDRCCLECQPGYGMVSRCNRSQDTICHPCEPGFYNEA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 VVIVLLLVGCEK----VGAV----QNSCDNCQPG----TFC-RKYNPVCKSCPPSTFSSI 55
                                                                                                                                        sono T., Seto A., Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 TPSAPYRPPTARTSTAWPRTAQGPSTP---TLEASKGPQLAIVLSLGLGLGLLALLAAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GGQPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCEKDCRPG-QELT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NOD;
Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
"Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice.";
Genomics 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 KQG--CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC-----
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Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
"Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Murine tumour necrosis factor receptor 2 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%; Score 183.5; DB 6; Length ; ilarity 27.8%; Pred. No. 1.4e-10; Conservative 22; Mismatches 103; Indels
                                                                                                                                                                                             T cell lines.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AB003911; BAA20059.1; -.
HSSP; Q92956; 1JMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28489 MW; A8B4CD3173C9500B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 ITLLFSVLKWIRKKFP--HIFKQPFKKTTGAAQEEDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALYLHORAWRPPKLPGGGSFRTPI-----OEEOA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA.
                                                                                                                                                                                                                                                                                               GO; GO: 000487; F: receptor activity; IEA. InterPro; IPR001368; TNFR_C6.

Pfam; PF00020; TNFR_C6; 3.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_2; 2.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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19 2
267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 77; Conserv
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                                                                                 FROM N.A.
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                         NCBI_TaxID=9986;
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                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
NON TER
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 -GVCRPWINCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 FEKCYPWISCEDKNLEVLOKGISOTNVICG------------ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 FLALTSALLLALI -- FITLLFSVLKWIRKKFPHIFKQPFKK--TTGAAQEEDACSCRCPQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNCQPGTFCRKY----NPVCKSCPPSTFSSIGGQP-NCNICRVCAGY--FRFKKFCSS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDLCOPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
0X40 precursor (Fragment).
0Xyctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                      Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
ol-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to tumor necrosis factor receptor superfamily, member 5.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%; Score 185.5; DB 11; Length 289; 25.1%; Pred. No. 9.3e-11; ive 33; Mismatches 88; Indels 61;
                                                                                                                                                                                                                                                                                                        Strausberg R.;

Strausberg R.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0005840; C:ribosome; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003775; F:structural constituent of ribosome; IEA.

R GO; GO:0004888; F:structural constituent of ribosome; IEA.

R GO; GO:0006915; P:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00962; RIBOSOMAL S2 1; 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 4.
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=10090;
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SEQUENCE
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EMBL; Y14620; CAA74969.1; -.
EMBL; Y14621; CAA74969.1; JOINED.
EMBL; Y14622; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
EMBL; Y14679; CAA74969.1; JOINED.
HSSP; Q92956; JUMA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam: PF00020; TNFR_c6; 4.
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PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                  Conservative
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                                                                 457 AA;
                                                                                                                                                                  Local Similarity
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       Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 FND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP--PVVSFSPSTTISVTP---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 ----EGGP------GGHSLQVLTLFLALTSALLLALIFILLES 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPI-GLIVGVTS---LGLLMLGLVNC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDGVETRAC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| :| |||| | ||:
156 FSDTTSSTDVCRPHRICSI----LAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 SSTHNAECECIEGFHCL-----CAPQCTRCEXDCRPGQELTKQG-----CKTCSLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONSCDNCOPGT --- FCRK-YNPVCKSCPPSTFSSIGGO-PNCNIC-RVCAGYFRFXKFC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to tumor necrosis factor receptor superfamily, member 1B
                                                                                           PIR; 148852, LOGF.
HSSP; P19438; INCF.
MGD; MGI:1314883; Thfrsflb.
GO; GO:0007166; P:cell surface receptor linked signal transdu.
GO; GO:0008220; P:inflammatory response; IMP.
GO; GO:0008220; P:inflammatory response; IMP.
InterPro; IPR001368; TNFR_GG.
InterPro; IPR001368; TNFR_GG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 182; DB 11; Length 459; 26.6%; Pred. No. 3.5e-10; tive 25; Mismatches 109; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC042167; AAH42167.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR C6.
Pfam; PF00020; TNFR C6, 4.
SWART; SM00208; TNFR, 3.
PROSITE; PS00652; TNFR NGFR 1; 1.
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93 93 T -> I.
268 268 F -> I.
345 345 S -> F.
421 421 Y -> C.
459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;
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Pfam; PF00020; TNFR c6; 4.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR 2; 3.
                          Manm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
PIR; 148854; 148854.
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TISSUE=Muscle;
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Best Local Simi
Matches 76;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                102 ETQACTREQNRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCA
                                                                                                                                                                                                                                                                                                                                                                                                                        121 LGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 -----GPPVVSFSPSTTI----SVTPEGGPGGHSLQVLTLFLALTSALLLALIFIT
                                                                                                                                                                                            20 KVGAVQNSCDNCQPG----TFCRK-YNPVCKSCPPSTFSSI-GGQPNCNIC-RVCAGYFR
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98414512; PubMed=9740674;
Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure and Characterization of the two Transcripts.";
Genomics 52:79-98(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                           70;
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                                                                                   Length 457;
                                                                            12.7%; Score 181; DB 4; Length 45' 25.4%; Pred. No. 4.4e-10; cive 36; Mismatches 102; Indels
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1
48120 MW; 1B634BBF1F5D77AC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 CV--IMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQ 313
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Best Local Similarity
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                                                                                                                                                                                                 NCBI_TaxID=9534;
                       01-NOV-1999
01-JUN-2003
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Q90W71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 TDRECTCLSGTFQINDTCVPYTV-CPVGWGVRKKGTETEDVRCKPCLRGTFSDVPSSVMK 170
                                     KTCSLGTFND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP--PVVSFSPSTTISV 173
                                                                                                                           171 KACAPGTFSDTTSSTDVCRPHRICSI----LAIPGNASTDAVCAPESPTLSAIPRTLYVS 226
                                                                                                                                                                            227 QPEPTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPI-GLIVGVTS---LGLL 282
        FRFKKFCSSTHNAECECIEGFHCL-----GPQCTRCEKDCRPGQELTKQG-----C 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNCOPGTFCRKYNP----VCKSCPPSTFSS-IGGOPNCNICR-VCAGYFRFKKFCSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Death receptor 6.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                203 FITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQBEDACSCRCPQEEEGGGGGYE 255
                                                                                                                                                                                                                                                                                                        283 MLGLVNCFILVQRKKKP-----SCLQRDAKVPHVPDEKSQDAVGLE 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 180; DB 13; Length 651; 30.6%; Pred. No. 8.1e-10; ive 22; Mismatches 71; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bridgham J.T., Johnson A.L.;
"Expression of DR6 in the ovary.";
submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF349908; AAK29666.2; -.
PIR; JC7705; JC7705.
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Last annotation update)
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GO; GO: 0004872; F: receptor activity; IEA.
GO; GO: 0007165; P: signal transduction; IEA.
InterPro; IPR001488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00005; DEATH DOMAIN; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           651 AA
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SEQUENCE
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            71
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Q9XSZ8
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PRELIMINARY;

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WEDLINE=99296730; PubMed=10366573;

WEDLINE=99296730; PubMed=10366573;

WEDLINE=99296730; PubMed=10366573;

WEDLINE=99296730; PubMed=10366573;

Theoretional characterization of the HveA homolog specified by African green fluorescence protein.";

Treen monkey kidney cells with a herpes simplex virus expressing the green fluorescence protein.";

Virology 258:365-374(1999).

RESP; Q2956; JJMA.

GO; GO:0006915; Paransmembrane receptor activity; IEA.

GO; GO:0006915; Pinmune response; IEA.

GO; GO:0006915; Pinmune response; IEA.

GO; GO:0006915; Pinmune response; IEA.

GO; GO:0006915; Pinmune response; IEA.

RO; GO:0007165; Pisignal transduction; IEA.

InterPro; IPR008063; Fas receptor.

BRINTS; PR01680; FASRECEPTOR.

ROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS00652; TNFR NGFR 2; 2.

SEQUENCE 283 AA; 30199 NW; 397951C6617FE3AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 F-SSIGGOPNONICRVC--AGYFRFKKFCSSTHNAECECIEGFHCL---GPOCTRCE--K 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 YIAHFNGLSKCLQCQMCDPAMGLRTSRNCSTTANALCGCSFGHFCIIQDGDHCAACRAYA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TSSPGQRVQKGGTESQDTLCQNCPPGTFSSNGTLEECQHGNKCSK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 VCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFL--ALTSALLLALIFITLLFSVLXWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGNNCYNVVVIVLLLVGCEK----VGAVQNSCDNCQPGTFCR----KYNPVCKSCPPST
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
101-JUN-2003 (Rainbow trout) (Salmo gairdneri).
101-JUN-2004 (Rainbow trout) (Salmo gairdneri).
101-JUN-2004 (Rainbow trout) (Salmoniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
101-JUN-2004 (Rainbow trout) (Salmoniformes; Salmonidae; Oncorhynchus.
101-JUN-2004 (Rainbow trout) (Salmoniformes; Salmonidae; Oncorhynchus.
101-JUN-2003 (TrEMBLRel. 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last December 19, Last Decemb
                                                                                                                                                                                           Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 RKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
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134 IATGISDTICDPCPIGFFSNVSSALEKCHPWTSCETKGLVKVQAGTNKTDVICGPQ---- 189
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                221 -IFKOPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                               Z
                                                                                                                         234 DLEEFPMPPHSIAPVQETLHGCQPVTQEDG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Virol. 75:226-233(2001).

EMBL; AJZ72008; CAC15562.1; -.

HSSP; P19438; 1EXT.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR.c6.
Ffam; PF000209; TNFR,c6, 2.

SMART; SM00208; TNFR, 2.

PROSITE; PS00652; TNFR.NGFR.1; 2.

PROSITE; PS50050; TNFR.NGFR.2; 2.

SEQUENCE 167 AA; 18500 NW; FB790E7927F9
                                                                                                                                                                                               167
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16,
24,
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01-MAR-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                        Cowpox virus (CPV)
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Orthopoxvirus.
NCBI_TaxID=10243;
                                                                                                                                                                                                                                                               CrmE protein.
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                                                                                                                                                                 RESULT 18
Q9DJL2
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Matches
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Q7ZZYS
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                                                                                                                                                                                                                                                                                                                                                                     103 KDCRPGQELTKQG-----CKTCSLGTFND-QNGTGVCRPWTNCSLDGRSVLKTGTTEK 154
                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ERHCHQHKYCDPNLGLHVEKEGTSETDTTCTCDEGLHCTNAACESCTMHSLCPPGLGVKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --QELIKQGCKTCSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 EPRTACREKQYLVDSQCCNMCPP-----GEKLVNDCLHTIDTECTRCQTGEFLDTWNA 73
                                                                                                                                                                                                                                                                                                                  4 NCYNVVVIVLLLVGCEKVGAVQN------SCDNCQPGTFCRKY----NPVC
                                                                                                                                                                                                                                                                                                                                                    45 KSCPPSTFSSIGGO-PNCNIC-RVCAGYFRFKKFCSSTHNAECECIEGFHCLGPQCTRCE
                     TISSUE=Leukocyte;

Pleguezuelos O., Secombes C.J.;
Pleguezuelos O., Secombes C.J.;
Pleguezuelos O., Secombes C.J.;

Roreening a rainbow trout (Oncorhynchus mykiss) cDNA library.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ315137; CAC43329.1; -.

R GO; GO:0004872; F:receptor activity; IEA.

IN THERPRO; IPR001368; TNFR c6.

R Pfam; PF00020; TNFR c6.

R Pfam; PF00020; TNFR; 3.

R SMART; SM00208; TNFR; 3.

R PROSITE; PS01186; EGF 2; 1.

PROSITE; PS00165; TNFR NGFR 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 QPGTFCRKY-----NPVCKSCPPSTFSSIGGQPNCNIC-------RVCAGYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79;
                                                                                                                                                                                                                                            12.3%; Score 176; DB 13; Length 285; 26.2%; Pred. No. 8.7e-10; ative 27; Mismatches 90; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 274;
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Yang S., Sim G.-K.;
"Canine CD40 and CD40 Ligand cDNA Sequences.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY333789; AAP86653.1; -.
SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;
                                                                                                                                                                                                                 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVCGPPVVSFSPSTIISVTPEGGP--GGH----SLQVLT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVYC-----SACTNGSRTHEGEAICDGELMEFLSLQILT 216
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.2:
Matches 58; Conservative
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[1]
SEQUENCE FROM N.A.
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les 61; Conserv
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01-OCT-2003 (
01-OCT-2003 (
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Matches
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6
    220
                               50 STPSSI-GGQPNCNICRVCAGYFRFKKF-CSSTHNAECECIEGFHCL----GPQCTRCEK 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VVIVL-----CRKY-NPVCKSCPP 49
166 SPSTIISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=elephantpox;
MEDLINE=20569353; PubMed=11119592;
Saraiva M., Alcami A.;
"CrmE, a novel soluble tumour necrosis factor receptor encoded :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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12.1%; Score 173; DB 12; Length 1.
1 Similarity 30.7%; Pred. No. 1e-09;
50; Conservative 22; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 KTKCGRGYGKKGEDEMGNTICKKCRKGTYSDIVSDSDQCKPMT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 DCRPGOELTKOG-----CKTCSLGTFND-QNGTGVCRPWT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FB790E7927F91680 CRC64;
                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Decoy receptor 3 (Fragment).
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67
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Q8VC17
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Best Local Similarity 23.1%; Pred. No. 2.5e-09;
Matches 65; Conservative 38; Mismatches 96; Indels 82; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 YMNYLEKCLYCNVXCGERQVEVQQCNATHNRACQCQEGFHAEMEFCVQ-HSEXXPGSGVV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 IGGQ-PNCNICRVCAGYFRFK-KFCSSTHWAECECIEGFHCLGPQCTRCEXDCRPGQELT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LLLLLABLGCSSPPTYQWRDAGTKERVTCQQCPPGTFVAQHCTKERPTVCAPCPDLHYTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 VVIVILLVGCEKVGAVQ-----NSCDNCQPGTF----CRKYNP-VCKSCPPSTFSS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 DNCQPGTFCRKYNPVCKSCPP-------STFS-SIGGQPNCNICRV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SI:dZ107D16.1 (Novel protein similar to vertebrate nerve growth factor receptor (NGFR)) (Fragment).
SI:DZ107D16.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SI:DZ107D16.1.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 172.5; DB 13; Length 186; 28.8%; Pred. No. 1.3e-09; Live 23; Mismatches 66; Indels 25;
                                                   SEQUENCE FROM N.A.

Bridgham J.T., Johnson A.L.;

Rocal expression in the hen.";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY251406; AAP03889.1;

GO; GO:004872; F:receptor activity; IEA.

InterPro; IPR006209; EGF like.

R InterPro; IPR001368; TNFR c6.

R Pfam; PF00020; TNFR; 4.

R PROSITE; PS0186; EGF 2; 1.

R PROSITE; PS01652; TNFR NGFR 1; 1.

R PROSITE; PS00052; TNFR NGFR 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramsay H.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 AA; 20671 MW; 31D65731DACB758E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 317 317
317 AA; 34446 MW; D9B7EF1C70DAF92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 KOG-----CKTCSLGTF-NDONGTGVCRPWTNCSLDGR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL591671; CAD43421.1; -... GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001368; TNFR c6.
Ffam; PF00020; TNFR c6; 4.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01086; TNFR; 4.
PROSITE; PS00652; TNFR NGFR 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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NCBI_TaxID=7955;
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  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
NON TER
SEQUENCE
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NON TER
SEQUENCE
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OX RARA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERNA BERN
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11;
                                                                                                                                                                                                                                                                         133 ECRDETYSDQENTWDPCMPCTICEEDTEILLRNCTPTEDALCHDPL---SPTYPTSTGDS 189
                                                                                                    CAGYFRFKKFCSSTHNAECECIEGF--HCLGPQCTRCEKDCRPGQ-----ELTKQG-CK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 ---GPQCTRC--EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 NODGSHCSTCLQHTTCPPGQRVEKRGTHDQDTVCADCLIGTFSLGGTQEECLPWTNCSAF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG-GPGGHSLQVLTLFLALTSALLLAL 201
15 BECESGSFTHS-GECCVQCPPGEGVIKECGATQTECTQCLDSETFSATFSHTDKCQVCTE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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190 GSFDTDLDRLWSPSPGDDATTPKPSSPHFIGRGLNENLIPIYCSILAAVVVGL-----
                                                                                                                                                                                                                                  118 TCSLGTFNDQNGT-GVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPE
                                                                                                                                                                                                                                                                                                                                                               G-----GPG-----GPG-----GHSLQVLTLFLALTSALLLALIFITLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 TFCRKYNPVCKSCPPSTFSSIGGOPNCNICRVCAGYFRFKKFCSSTHNAECECIEGFHCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.0%; Score 171.5; DB 11; Length 196; Best Local Similarity 27.2%; Pred. No. 1.7e-09; Matches 62; Conservative 22; Mismatches 87; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 IFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 -----SŸVAKEL-----EPFQ------ÒEQQENTIRPPVTEVG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
E Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
E EMBL; BC022125; AAH22125.1; -.

R GO; GO:0004915; P:combrane; IEA.
GO; GO:0006915; P:sapoptosis; IEA.
GO; GO:0006915; P:signal transduction; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R InterPro; IPR008063; Fas receptor.
R InterPro; IPR001368; TNFR C6.
R Pfam; PF00209; TNFR C6. 3.
R PRINTS; PR01680; TNFR C6. 3.
R PROSITE; PS50050; TNFR J.
N Hypothetical protein.
I NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 SVLKWIRKKFPHIFKQ--PFKKTTGAAQEEDACSCRCPQEE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 --LAYI-----IFKRWNSCKONKOAANNRAATANQTPSPE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8VC17;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Liver;
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InterPro; IPR008063; Fas_receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS0050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 NGTGVCRPWTNCSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 LRNYRLDPFPPCKL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
01-NOV-1999
01-JUN-2003
                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                         Query Match
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Q9WJB4
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Matches
  SO PRESENTANT OF STANTANT OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 STFSSI-GGOPNCNICRVCAGYFRFKKF-CSSTHWAECECIEGFHCL----GPQCTRCEK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VVIVL------LLVGCEKVGAVQNS-----CDNCQPGTF----CRKY-NPVCKSCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                        RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reading P.C., Khanna A., Smith G.L.;

Reading P.C., Khanna A., Smith G.L.;

"Vaccinia virus CrmE encodes a soluble and cell-surface tumor necr
factor receptor that contributes to virus virulence.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AJ315962; CAC83048.1; -.

RO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR.c6.

R SMART; SM00208; TNFR, 3.

R SMART; SM00208; TNFR, 3.

R PROSITE; PS00652; TNFR NGFR 1; 2.

R PROSITE; PS50050; TNFR NGFR 2; 2.

R SEQUENCE 167 AA; 18510 MW; 384A0D4A27FB797D CRC64;
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Reading P.C., Khanna A., Smith G.L.;
"Vaccinia virus encodes a soluble and cell surface tumour necrosis
factor receptor that contributes to viral virulence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.0%; Score 171; DB 12; Length 167; 30.7%; Pred. No. 1.6e-09; ive 22; Mismatches 57; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 DCRPGQELTKQG-----CKTCSLGTFND-QNGTGVCRPWT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 0:0-0(0).

EMBL; AJ416893; CAC95181.2; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004888; F:transmembrane receptor activity; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0007165; P:signal transduction; IEA.
                                                                                                                                                                                 Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                        167 AA
                                                                                                                                                       Created)
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                                                                                                                                          01-MAR-2002 (TrEMBLrel, 20, 01-MAR-2002 (TrEMBLrel, 20, 01-JUN-2003 (TrEMBLrel, 24,
                                                                                                                                                                                                                                                                                                                                             no
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                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                      Vaccinia virus.
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Orthopoxvirus.
NCBI_TaxID=10245;
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                                                                                                                                                                                                                                          CrmE protein.
CRME.
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                                                                                Q8UYL3
               RESULT 22
QBUYL3
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51 CNRCPPGEFAKVRCNGNDNTKCERCPPHTYTAIPNYSNGCHOCKKCPTGSFD-KVKCTGT 109
                                                                                                                                                                                                                                                                                                        81 HNAECECIEGFHCL--GPQCTRCEKDCRPGQE-----LTKQG---CKTCSLGTFNDQ 127
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                                                                                                                                                                                 28 CDNCOPGTFCR----KYNPVCKSCPPSTFSSIGGOPN-CNICRVC-AGYFRFKKFCSST
                                                                                                                            22; Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Lister;
MEDLINE=99226947; PubMed=10211965;
Alcami A., Khanna A., Paul N., Smith J.L.;
"Vaccinia virus strains Lister, USSR and Evans express soluble and cell-surface tumour necrosis factor receptors.";
J. Gen. Virol. 80:949-959(1999).
EMBL; X17728; CAB41042.1;
HSSP; Q92956; LJMA.
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                                                                 Length 186;
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                                                                                                                         49; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
Interpro; IPR001803; FAS receptor.
Interpro; IPR001803; TNFR.c6; C.
Pfam; PF000203; TNFR.c6; C.
PRINTS; PR01680; PASRECEPTOR.
SMART; SM00208; TNFR, 2.
PROSITE; PS00652; TNFR, NGFR.1; 2.
PROSITE; PS00652; TNFR.NGFR.2; 2.
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186 AA; 20662 MW; EF73D6A336A70C5A CRC64;
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SEQUENCE 186 AA; 20646 MW; D83CD9180276EE31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                       / Match 11.8%; Score 169; DB 12; Local Similarity 31.3%; Pred. No. 2.9e-09; Nes 42; Conservative 21; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor receptor precursor.
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66 GPCPKSHYTEIWNYIERCQYCNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSR-H 124
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125 RRCPPGEGVISNGTAHTDVKCEPCPVGFFSAVSSSRKACQKFSVCP-PGRITI-PGNDMN 182
103 KDCRPGQELTKOG-----CKTCSLGTRND-QNGTGVCRPWTNCSLDGRSVLKTGTTEK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 NCYNVVIVILLVGCEKVGAVQN------SCDNCQPGTFCRKY----NPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 NCFLPLLVFALCGGSVPVSGAHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu L., Fujiki K., Dixon B., Sundick R.S.;
"Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine with a fractalkine-like stalk and a TNF decoy receptor using cDNA fragments containing AU-rich elements.";
Submitted (UIL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF401631; AAK91758.1;
GO: GO: 0004872; F: receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001369; TNFR c6.
Pfam; PF00020; TNFR c6.
                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TNF decoy receptor.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 DVVCGPPVVSFSPSTTISVTPEGGP--GGH-----SLQVLT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 DVYC-----SACRNGSRTHEGQAICDGELMEFLSLQILT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 AA; 31795 MW; SE3BD1B6EFC6BABC CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                 PRT;
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19,
                                                                          128 NGTGVCRPWTNCSL 141
                                                                                                                     169 LRNYRLDPFPPCKL 182
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                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8022;
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
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SEQUENCE
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Matches 5
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                                                     81 HNAECECIEGFHCL--GPQCTRCEKDCRPGQE-----LTKQG---CKTCSLGTFNDQ 127
                        81 HNAECECIEGFHCL--GPQCTRCEKDCRPGQE-----LTKQG---CKTCSLGTFNDQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=GRI-90;
MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
"Species-specific differences in genome organization of cowpox,
smallpox, and vaccinia viruses.";
Virology 243:432-460(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V., Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J., Sandakhchiev L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GRI-90;
MEDLINE=97068532; PubMed=8963248;
Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V., Shchelkunov S.N., Sandakhchiev L.S.;
"Genes of a circle of hosts for the cowpox virus.";
Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Totmenin A.V.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; X94355; CAD90723.1; -.
HSSP; Q92956; LJMA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 2.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50050; TNFR NGFR 2; 2.
SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                186 AA.
                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                     128 NGTGVCRPWTNCSL 141
                                                                                                                                                                      169 LRNYRLDPFPPCKL 182
                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=GRI-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orthopoxvirus.
NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                     A56R protein.
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SEQUENCE FROM N.A
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                             Query Match
Best Local S
Matches 40
       SEQUENCE
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                                                                                                                                                                                                                                           RESULT 29
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                                                                                                                                                                                                                                                                                                                                              73 FK-----KFC------SSTHNAECECIEGFHCLGPOCTRC--EKDCRPG---- 108
                                                                                                                                                                                                                                                                                                                                                                       74 EKHCHQHKYCDPNLGLQVQREGTSKTDTTCVCSEGHHCTNSACESCTLHSLCFPGLGVKQ 133
                                                                                                                                                                                                                                                                                                                                                                                               109 --QELTKQGCKTCSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSF 165
                                                                                                                                                                                                                                                                                                                                                                                                             21 EPPTSCKENQYPINSRCCNLCPP-----GQKLVNHCTEVTETECLPCSSSEFLATWNR 73
                                                                                                                                                                                                                                                                           83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20111091; PubMed=10642582;
Bobe J., Goetz F.W.;
"A tumor necrosis factor decoy receptor homologue is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salvelinus fontinalis (Brook trout) (Brook char).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protaganthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                11.7%; Score 167.5; DB 6; Length 278; 24.3%; Pred. No. 6.3e-09; ive 24; Mismatches 64; Indels 83;
       Nest K.A., Li A.W., Rowden G.;

West K.A., Li A.W., Rowden G.;

West K.A., Li A.W., Rowden G.;

"Characterization of the Porcine CD40 Molecule.";

L Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0004888; F:transmembrane receptor activity; IEA.

R GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR0008063; Fas receptor.

R InterPro; IPR001368; TNFR C6.

R PRINTS; PR01680; FASRECEPTOR.

R PROSITE; PS00652; TNFR, 4.

R PROSITE; PS00652; TNFR NGFR 1; 1.

R PROSITE; PS00652; TNFR NGFR 1; 1.

R PROSITE; PS00652; TNFR NGFR 2; 4.

SEQUENCE 278 AA; 30951 MW; 20D446E44AF93DD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 SPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                               OPGTFCRK-----YNPVCKSCPPSTFSSIGGOPNCNIC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0004872; F: receptor activity; IEA. InterPro; IPR006209; EGF like. InterPro; IPR001368; TNFR c6.
Fam; PF00020; TNFR c6; 4.
SMART; SM00208; TNFR; 4.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
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EMBL; AF156738; AAD56428.1; -.
HSSP; O14763; 1D4V.
                                                                                                                                                                                                                                                          Local Similarity 24.3% les 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Decoy TNF receptor
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82 NAECECIEGFHCLGPQCTRC--EKDCRPGQELTKQG-----CKTCSLGTFND-QNGTG 131
                                                                                                                                                                                                                                                                                                                                 96 NCECECKEGYY-FNKKYEACIKHKECPPGYGANTIGTPHQDTECVQCQAGFYSEVSSAKA 154
                                                                                                                                                                  28 CDNCQPGTFCR----KYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKFCSSTH 81
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Brighton Red;
MEDLINE=94378510; PubMed=8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";
Virology 204:343-356 (1994).
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
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STRAIN=Brighton Red;
MEDLINE=83117629; PubMed=6961398;
Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
"Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
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STRAIN=Brighton Red;
MEDLINE=91196263; PubMed=2014645;
Hu F.Q., Pickup D.J.;
"Transcription of the terminal loop region of vaccinia virus DNA initiated from the telomere sequences directing DNA resolution.";
                                                                                                                   17;
                                                           DB 13; Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Brighton Red;
MEDLINE=90177240; PubMed=2309453;
Parsons B.L., Pickup D.J.;
"Transcription of orthopoxvirus telomeres at late times during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Brighton Redgene;
Smith C.A., Goodwin R.G., Pickup D.J.;
"Cowpox virus Encodes a second soluble INF receptor (CrmC)
                                                   11.6%; Score 165.5; DB 13; Length 27.2%; Pred. No. 1.1e-08; ive 20; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from CrmB.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
  E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Soluble TNF receptor CrmC (V183).
                                                                                                                                                                                                                                                                                                                                                                                                132 VCRPWTNCSLDGRSVLKTGTTEKDVVC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 TCLAQSNCKVGGLRVVLKGQDWHNTLC 181
34037 MW;
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                                                                             Similarity 27.2 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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302 AA;
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Cowpox virus (CPV).
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               401 AA;
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K3R.
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01-JUN-2003
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Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Hutson L.D., Richards A.P., Bothwell M.;

"Life and death in the developing Xenopus retina: The role of the p75 neurotrophin receptor.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF172400; AAD51031.1; -.

EMBL; AF172399; AAD51030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNCQPGTFCR----KYNPVCKSCPPSTFSSIGGQPN-CNICRVC-AGYFRFKKFCSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 186;
                                                                                                                         Pickup D.J.;
                                                                          SEQUENCE FROM N.A.
STRAIN=Brighton Red;
Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; US5052; AAD10325.1; -.
EMBL; AF82758; AAM13631.1; -.
R HSSP; Q92956; 1UMA.
R HSSP; Q92956; 1UMA.
InterPro; IPR001368; TNFR_C6.
R Fam; PF00020; TNFR_C6; 2.
R SMART; SM00208; TNFR_C6; 2.
R PROSITE; PS00652; TNFR_NGFR_1; 2.
R PROSITE; PS00652; TNFR_NGFR_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels
                       Pickup D.J.;
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                    186 AA; 20372 MW; FC720DA743F62A2A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
P75 neurotrophin receptor A-2.
                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 163; DB 12;
llarity 29.9%; Pred. No. 1.2e-08;
Conservative 21; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 AA
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
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SMART; SM000005; DEATH; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_1; 3.
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InterPro; IPR006209; EGF like.
InterPro; IPR001368; TNFR_c6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00531; death;
Pfam; PF00020; INFR C6
   STRAIN-Brighton Red
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
Les 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                               109 ----QELTKQGCKTCSLGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC---G 159
                                                                                                                                                                                                                                                                                                                                                            PPVVSFSPS------TTISVTPEGG----PGGHSLOVLTLFLALTSALL 198
                                                                                                                                                                                       64
                                                                                                                                        12 VLLLVGCEKVGAVQNS------CDNCQPG----TFCRKYNPVCKSCPPS-TFS
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 LALI-FITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQBEDACSCRCPQEEEGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EKRWNS-----CKONKOGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GRI-90;
MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
"Species-specific differences in genome organization of cowpox,
smallpox, and vaccinia viruses.";
Virology 243:432-460(1998).
                                                                                              87;
                                             Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V., Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J., Sandakhchiev L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V., Shchelkunov S.N., Sandakhchiev L.S.; "Genes of a circle of hosts for the cowpox virus."; Dokl. Akad. Nauk 349:829-833(1996).
                                             %; Score 161.5; DB 13; Length
%; Pred. No. 3.9e-08;
37; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Totmenin A.V.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; X94355; CAD90751.1; -.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
D13BCAF7863EFECF CRC64;
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Last sequence update)
Last annotation update)
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MEDLINE=97068532; PubMed=8963248;
   43419 MW;
                                                   11.3%;
22.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 AGLVAFIV------
                                   Query Match
Best Local Similarity 22.9%
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66; Conservative
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                                                       -----EGGb-
                                                                                                                                                                                        209 SVLKWIRKK-
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SEQUENCE
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Q8WMQ2;
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Q8WMQ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 STFSSI-GGOPNCNICRVCAGYFRFKKF-CSSTHNAECECIEGFHCL----GPOCTRCEK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 -CSSTHNAECECIEGFHCL----GPQCTRCEK--DCRPG----QELTKQG---CKTCSLG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 NCTKKQNRVCACNADSYCALKIHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFND-QNGTGVCRPWTNCSLDGRSVLXTGTTEXDVVCG--PPVVSFSPSTTISVTP---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFSDTISSIDVCRPHRICSI----LAIPGNASTDAVCASESPIPSAVPRIIYVSQPEPTR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 WIVL------CRKY-NPVCKSCPP 49
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C STRAIN—Spreadue-Dawley;

C STRAIN—Spreadue-Dawley;

Schomburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;

Suburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMCCAKCPPGOYAKHFCNKTSDTVCADCAAGMFTQVWN--HLHTCLSCSSSCSDDQVETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                         Query Match 11.3%; Score 161; DB 12; Length 167; Best Local Similarity 30.1%; Pred. No. 1.7e-08; Matches 49; Conservative 22; Mismatches 58; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 DCRPGQELTKQG-----CKTCSLGTFND-QNGTGVCRPWT 137
HSSP; P19438; 1EXT.
GO; GO:0004872; F:receptor activity; 1EA.
InterPro; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR.NGFR.1; 2.
PROSITE; PS0050; TNFR.NGFR.2; 2.
SEQUENCE 167 AA; 18526 MW; 3B4A0D5A67F73961 CRC64;
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1 Similarity 24.9%; Pred. No. 6e-08;
69; Conservative 26; Mismatches 106;
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 24, Last ann
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SEQUENCE
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Best Local (
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Q91ZM6
ID Q91ZMA
AC Q91ZMD 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
COC MAMME OS
NCBI
RP SEQUE
RC STRAIL
RP SEQUE
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206 SQPMDQEPGPSQTPHIPVSLGSTPIIEPSITGGISLPI-GLIVGLTT---LGLLMLGLAN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 -CSSTHNAECECIEGFHCL---GPQCTRCEK--DCRPG----QELTKQG---CKTCSLG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 TFSDTTSSTDVCRPHRICSI----LAIPGNASTDAVCASESPTPSAVPRIIVVSQPEPTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCG--PPVVSFSPSTTISVTP---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 SQPMDQEPGPSQTPHIPVSLGSTPIIEPSITGGISLPI-GLIVGLTT---LGLLMLGLAN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 QNSCDNCQPGT----FCRK-YNPVCKSCPPSTFSSIGGQPNCNICRVCAGYFRFKKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Membrane protein CD40 (Fragment).
Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 158; DB 11; Length 474; 26.3%; Pred. No. 1.1e-07; cive 22; Mismatches 97; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Spleen;
Li Y., Ji A., Schafer M.K.;
Li Y., Ji A., Schafer M.K.;
"Expression of TNFR2 in rat dorsal root ganglion.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF498039; AAP33151.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_C6.
R SMART; SM00208; TNFR; 4.
R SMART; SM00208; TNFR; 4.
R PROSITE; PS500652; TNFR_NGFR_1; 2.
R PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                            262 CFILVQRKKPSCLQRETMVPHLPDEKSQDAVGLEQQ 298
                                                                                                                                                                                                                                                                                                                                          474 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor receptor type II
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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SO OR SO OR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 W-------TNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG-- 180
                                                          76 FCSSTHNAECECIEGFHCLGPQCTRC--EKDCRPGQELTKQG------CKTCSLGTFND 126
                                                                                       43
103 ----KDCRPGQ-----CRP-CRP-CRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 GHWGFPTCRPCQCNGHAEECDPQTGSCLRCRDHTDGERCQRCAAGHFGNPALGSGQHCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 FHTVVLSPVAEPCSRLLHSLSAILHNGALPCLCDPOGSLSAECOPOGGOCKCKPNVVGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      808 CHRCSPGTFGF--GPRRCDPCQ-CSGEGSLSAVC-DIVIGQCPCRQGAH--GSRCDRCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 YNVWVIVLLLVGCEKV-----GAVQNSCD-----NCQP-GTFCR-KYNPV---
                                                                                                                                                                                                                                                                                                                             Ol-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 24, Last annotation update)
Laminin beta 2-like chain.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98209634; PubMed=9550264;
Liu J., Swasdison S., Xie W., Brewton R.G., Mayne R.;
Liu J., Swasdison S., Xie W., Brewton R.G., Mayne R.;
"Primary structure and expression of a chicken laminin beta chain:
evidence for four beta chains in birds.";
Matrix Biol. 16:471-481(1998).
EMBL; AF038555; AAB92586.1; -.
HSSP; P02468; 1KLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 152; DB 13; Length 1792; 27.3%; Pred. No. 1.8e-06; ive 20; Mismatches 74; Indels 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1792 AA; 195723 MW; 4A4CBE0206F6A600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO: 0005578; C:extracellular matrix; IEA.
GO; GO:0005588; F:structural molecule activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR008211; Laminin_EGF.
InterPro; IPR008211; LamNT.
Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nerm; 1.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00180; EGF_Lam; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D'Rear J.J.;
"A novel laminin B1 chain variant in avian eye.";
J. Biol. Chem. 267:20555-20557(1992).
                                                                                                                                                                                      138 FNDAFTHCOSHTRCGDLGKEVKSAGTETTDAVCG 171
                                                                                                                                              127 ONGIGY-CRPWINCSLDGRSVLKTGTIEKDVVCG
                                                                                                                                                                                                                                                                                              PRT; 1792 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS000136; LamNT; 1.
PROSITE; PS00022; EGF 1; 10.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Laminin_EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=93015947; PubMed=1400373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 27.3
hes 67; Conservative
                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 67,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 VQNSCDNCQPGTFCR----KYNPVCKSCPPSTFSS-IGGQPNCNICRVCAGYFRFK--K 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Head kidney;
Zou J., Secombes C.J.;
Molecular cloning and expression analysis of a TNF receptor homologue in rainbow trout, Oncorhynchus mykiss.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ517804; CAD57165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNCOPG----TFCRKYNPV-CKSCPPSTF-SSIGGOPNCNICRVCAGYFRFKKFCSSTH
                                                                                           SEQUENCE FROM N.A.

Zawitkowski M.S., Russ G.R., Krishnan R.;

"Cloning and expression of the ovine CD40 molecule and the inhibition of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
        Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Indels
                                                                                                                                                                               protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                               EMBL; AX072798; AAL68402.1; -. GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 AA; 35254 MW; 78F8135011283B43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%; Score 155; DB 6; 29.3%; Pred. No. 1.2e-07; tive 15; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEKCHPWISCERKGLVEQHVGINKIDAVCG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 TGVCRPWTNCSLDGRSVLKTGTTEKDVVCG 159
                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00020; TNFR C6; 4.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
NON TER 277 277
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Best Local Similarity 29.5.
Local 44; Conservative
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                                Bovidae; Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 40; Conserv
                                                 NCBI_TaxID=9940;
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01-OCT-2003
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SEQUENCE
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PRELIMINARY;
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SI:DZ94E17.1.
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                                                                                                                                                                                                                                                                QBJFU6;
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Q8LRM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNCOPG----TPCRKYNPV-CKSCPPSTFSSIGGOP-NCNICRVCA--GYFRFKKFCSS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 CDLCOPGNRLVSHCTALEKTOCOPCDSGEFSAHWNREIRCHOHRHCELNQGLOVKKEGTA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 62-169 FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
MEDLINE=99330195; PubMed=10403401;
Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer and activator of transcription-1.";
FEBS Lett. 453:191-196(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005622; C:intracellular; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005840; C:ribosome; IEA.

GO; GO:0004888; F:structural constituent of ribosome; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:immune response; IEA.

GO; GO:0006412; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR008063; Fas_receptor.

InterPro; IPR001865; Ribosomal_S2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
Gao D., Hecker M.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241231; AAF43717.2; -..
HSSP; Q92956; 1JMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18525 MW; F199D91EFA224A26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 15, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00962; RIBOSOMAL S2 1; 1. PROSITE; PS00652; TNFR NGFR 1; 1. PROSITE; PS50050; TNFR NGFR 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00020, TNFR c6, 3-
PRINTS, PR01680, FASRECEPTOR.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (Fragment)
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169 AA;
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Best Local Similarity
Matches 40; Conserv
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51 TFS-SIGGOPNONICRVCAGYFRFKKFCSSTHNAECECIEGF--HCLGPQCTRCEKDCRP 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TFSATFSHTDKCQVCTECTGLMRMQTPCTDSNDAECVCNYGYFMNVLSSRCEPCTV-CPL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILAAVVVGL------LAYİ-----İFKRWNSCKONKQAANNRAATANQTPSPE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 60; Gaps
                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
81:4294E17.1 (Novel protein similar to nerve growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mastigoneme-like protein.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
NCBI TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lloyd D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL596203; CAD43457.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001368; TNFR G6.
Rem; PF00020; TNFR G6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00652; TNFR NGFR 1; 2.
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235 235
235 AA; 25783 MW; 7C6CA5FAFB16E7BE CRC64;
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Best Local Similarity 24.4%; Pred. No. 2.6e-07;
Matches 58; Conservative 35; Mismatches 85;
                                                                                                                                                                                                                                  235 AA
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131 GV---CRPWING 139
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SEQUENCE FROM N.A.
Song L., Dentler W.L.;
"Molecular cloning and characterization of a 240 kDa flagellar protein
in Chlamydomonas.";
                                                                                                                                                                                                                                                                                                                                                                                                                      28 CDNCQPGTFCRKYN-PVCKSCPPSTFSSIGGOPNCNICR-----VCA------
                                                                                                                                                                                                                                                                                                               Query Match 10.5%; Score 149.5; DB 10; Length 1997; Best Local Similarity 26.5%; Pred. No. 3.7e-06; Matches 53; Conservative 24; Mismatches 64; Indels 59;
                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF508983; AAM33652.1; -.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000209; Peptidase S8.
PROSITE; PS00136; SUBTILASE ASP; 1.
SEQUENCE 1997 AA; 206459 WW; A4061C41FEAA7047 CRC64;
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Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; Last sequence update) Last annotation update) 573 AA Created) PRT; 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Death receptor 6. TNFRSF21 OR AA959878. PRELIMINARY; RESULT 40
Q8BZU6
TD Q8BZU
AC Q8BZU
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
STRAIN=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).

Query Match
Best Local Similarity 29.9%; Pred. No. 2e-06;
Matches 50; Conservative 18; Mismatches 64; Indels 35; Gaps EMBL; AK033529; BAC28342.1; -.

MGD; MGI:2151075; Thfrsf21.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR001368; Death.

R Pfam; PF00521; death; 1.

R Pfam; PF00020; TNFR_C6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00005; DEATH; 1.

R PROSITE; PS00652; TNFR NGFR 1; 1.

R PROSITE; PS50050; TNFR NGFR 1; 1.

R PROSITE; PS50050; TNFR NGFR 2; 1.

R PROSITE; PS50050; TNFR NGFR 2; 1.

Search completed: May 5, 2004, 14:40:33 Job time: 89.6712 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model ı OM protein 5, 2004, 14:30:20 ; Search time 5.46233 Seconds (without alignments) 568.992 Million cell updates/sec Мау Run on:

US-10-067-122B-2_COPY_105_115 62 1 CRPGQELTKQG 11

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2003bs:* 29Jan04:* A Geneseq 1: geneseq Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	20	Aab66986 41bb prot	66	78	173 Mouse	Aaw26659 Mouse 4-1	83	112	in	5954	Adc25939 Murine re	Ade87549 Mouse rec	2882	Adc25944 Murine re	Aar74087 Human rec	714	Aaw31759 A novel h	Aaw92523 Human h4-	Aaw92524 Human h4-	Aae08545 Human h4-	39	5	Aar70977 H4-1BB re	Aaw04174 Human rec	Aaw26658 Human 4-1
ΩI	ADC25950	AAB66986	AAR64199	AAR70978	AAW04173	AAW26659	AAY28687	AAY33215	AAE22581	ABB75954	ADC25939	ADE87549	58	ADC25944	AAR74087	AAY94714	AAW31759	AAW92523	AAW92524	AAE08545	ABB84639	AAR64197	AAR70977	AAW04174	AAW26658
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ALIGNMENTS

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The invention relates to a novel CDNA gene encoding receptor protein 4-
1BB. The cDNA gene of the invention demonstrates immunostimulant
activities and may be useful as a probe to isolate DNA sequences encoding
for proteins similar to the receptor protein encoded by the DNA. The
protein, its fragments and derivatives may be useful as a probe to
isolate ligands to receptor protein 4-1BB, for stimulating proliferation
of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand
binding. The antibody may be useful for enhancing T-cell proliferation or
activation. Finally, the invention may be useful with respect to cancer
research. The current sequence is that of the murine receptor 4-1BB
peptide (residues 105-115) of the invention.
                                                                                                                                                            receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cDNA gene encoding receptor protein 4-1BB, useful for isolating similar DNA sequences, and the encoded polypeptide and an antibody to it, useful for identifying ligands, and for modulating immune cell activity.
                                                                                                                           Murine receptor 4-1BB peptide - residues 105-115.
                                                                                                                                                                                                                                                                                                                                                                                                                         (ADRE-) ADVANCED RES & TECHNOLOGY INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 22, 77pp, English.
                             ADC25950 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                      88US-00267577.
92US-00922996.
93US-00012269.
                                                                                                                                                                                                                                                                                                                        04-FEB-2002; 2002US-00067122.
                                                                                                 (first entry)
                                                                                                                                                                                  cancer; murine; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-678138/64.
                                                                                                                                                                                                                                                      JS2003100745-A1.
                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                                                                         37-NOV-1988;
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01-FEB-1993;
                                                                                                  18-DEC-2003
                                                                                                                                                                                                                                                                                      29-MAY-2003.
                                                                ADC25950;
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RESULT 1
                  ADC25950
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Sequence 11 AA;

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Gaps

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The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor—alpha inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple conditions leading to bone loss such as rheumatoid arthritis, multiple scalerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GvHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, bonnaries, commaniance of populary conditions (e.g. myocardial infarction) and septic shock. The present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                   Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.
Score 62; DB 7; Length 11; Pred. No. 0.0003; Mismatches 0; Indels
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                                                                                                                                                                                                                       AAB66986 standard; protein; 191 AA
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07-JUL-2000; 2000WO-US018667
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                                                                               1 CRPGOELTKOG 11
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                     Best Local Similarity
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09-DEC-1999;
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                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB to transduce signal.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                    T-cell; lymphocyte; activation; tissue culture; clone; cell lines; proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
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             100.0%; Score 62; DB 4; Length 191; 100.0%; Pred. No. 0.0055; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 44-45; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alderson MR;
                                                                                                                                                              AAR64199 standard; protein; 256 AA.
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(first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                         Murine 4-1BB polypeptide.
                                                                                            CRPGQELTKOG 115
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                    CRPGOELTKOG
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                                                                                                                                                                                                                                                                                                                             Mus musculus
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08-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1994.
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                                                                                             Monoclonal antibody specific for human receptor protein 4-1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating auto:immune diseases.
                                                                                                                                                                                Novel murine receptor protein 4-1BB (AAW04173) has the potential to function as an accessory signaling molecule during T-cell activation and proliferation. It may represent a cell surface molecule involved in T-cell-APC interactions and may also act as a B-cell costimulator. It is structurally related to members of the nerve growth factor receptor superfamily. Its amino acid sequence was deduced from an isolated cDNA clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was identified and used to raise a monoclonal antibody useful in cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell; proliferation; immunostimulant.
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                                                                                                                                                         Disclosure; Page 32-34; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith CA;
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/label= Sig_peptide
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(INDV ) UNIV INDIANA FOUND
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Best Local Similarity 100.
Matches 11; Conservative
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N-PSDB; AAT91027.
                                                        WPI; 1996-443138/44.
N-PSDB; AAT39541.
                              Kwon BS, Kang C;
                                                                                                                                                                                                                                                                                                                                     Sequence 256 AA;
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25-FEB-1998
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AAW26659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was isolated using PCR primers based on the homologous mouse 4-1BB gene (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                               Novel cDNA encoding human receptor protein H4-1BB - useful to produce the protein which is used to treat auto:immune disease and facilitate organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
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                                                              4-1BB; receptor protein; immunosuppressive; autoimmune disease; organ transplantation; cell membrane ligand.
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/label= Sig_peptide
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        (first entry)
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                                     4-1BB receptor protein
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        16-OCT-1995
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                                                                                                            Mus sp.
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This protein comprises mouse 4-1BB, a member of the tumour necrosis factor receptor superfamily that is expressed on helper, suppressor and cytolytic T cells, as well as on mouse brain tissue. A novel claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned and sequenced (see AAW26656) that binds to murine 4-1BB. 4-1BB-L, especially its soluble extracellular domain, can be used to stimulate T-cell proliferation in vitro, as a research tool and as an affinity ligand for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Receptor 4-1BB cDNA; Mouse Receptor 4-1BB protein; H4-1BB protein human 4-1BB protein; T cell activation; proliferation; immune response; receptor protein; autoimmune disease; organ transplantation; cancerous tumour; nerve growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 2; Length 256;
Pred. No. 0.0074;
Mismatches 0; Indels
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100.0%; Pri
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N-PSDB; AAX90763.
                                                                                                                                                                                                                                                                                                              Sequence 256 AA
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The present sequence is mouse 4-1BB receptor protein. This protein has 65% homology with human receptor protein 4-1BB. The protein has a putative leader sequence, a potential membrane anchor segment and other features of known receptor proteins. 4-1BB is structurally related to members of the nerve growth factor receptor. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation; for activation or inhibition of immune response; to block H4-1BB ligand binding; treating cancerous tumours and autoimmune diseases; and during Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus. Disclosure; Page 75; 86pp; English. organ transplantation

This invention describes a novel use of the human monocyte growth factor CD137, or its functional analogs, for (i) stimulating proliferation of peripheral monocytes; and (ii) treating diseases that are associated with disorders of a cellular system that includes monocytes (and/or their progression is treatable by stimulating proliferation of such cells. The products of the invention have antitumor, antibacterial, antivital, antifungal and immunostimulatory activity. Stimulating proliferation of monocytes promotes the non-specific immune response, i.e. it increases phagocytosis and intracellular destruction of microorganisms, immune complexes and damaged cells, and improves antibody (in) dependent cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat diseases associated with a defective immune response where caused by inadequate numbers of active monocytes/macrophages, especially damage to the hematopoietic system (leucopenia) caused by chemotherapy or radiation therapy; disorders of wound healing (e.g. in dialysis or diabetic patients, or those with chronic venous insufficiency); tumors; bacterial, fungal or viral infections; (non-)congenital or (non-)inherited diseases

fungal or viral infections; (non-) congenital or (non-) inherited diseases or injury to the immune system; injury induced by treatment with immunosuppressants (e.g. patients with chronic arthritis or autoimmune disease, or transplant patients). Nucleic acid encoding (I) can be used similarly, in gene therapy procedures. Proliferation of peripheral monocytes is achieved independently of hematopoietic stem cells. This sequence represents the murine CD137 protein described in the method of

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Sequence 256 AA
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                                                                                                                                                                                                   CD137; monocyte growth factor; proliferation; peripheral monocyte; treatment; disease; antitumor; antibacterial; antiviral; antifungal; immunostimulatory; non-specific immune response; phagocytosis; intracellular destruction; microorganism; immune complex; antibody; cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia; chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal; bacterial; viral infection; immunosuppressant; gene therapy; murine.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of monocyte growth factor CD137 for stimulating proliferation o peripheral monocytes, particularly for treating immune deficiency, following cancer therapy.
                      ;
   Length 256;
100.0%; Score 62; DB 2; Length 25 ilarity 100.0%; Pred. No. 0.0074; Conservative 0; Mismatches 0; Indels
                                                                                                                  AAY33215 standard; protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1B; 57pp; German.
                                                                                                                                                                                                                                                                                                                                                        99WO-EP001440.
                                                                                                                                                                                                                                                                                                                                                                            98EP-00103859
                                                                                                                                                             (first entry)
                                                               115
                                          1
                                          1 CRPGQELTKQG
                                                               105 CRPGOELTKOG
                                                                                                                                                                                Murine CD137 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-550983/46.
Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                            18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                       05-MAR-1999;
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The present sequence is the protein sequence of the murine cytokine receptor, 4-1BB. A portion of the extracellular (ligand binding) domain of the receptor was utilised in a murine 4-1BB/human 1gG1 Fc fusion protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see ABB75952). The invention provides novel murine and human 4-1BB-L polypeptides and human 4-1BB polypeptides, as well as DNA sequences encoding them, recombinant expression vectors and host cells, and methods for producing the novel polypeptides by cultivating the transformed host cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from their extracellular domains, have therapeutic value. Antibodies that are immunoreactive with 4-1BB-L or human 4-1BB are claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody specific for the cytokine 4-1BB-ligand, useful for immunoaffinity purification of the ligand.
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                                                                                                                                                                                                                                                                                                                                                                                       24. .256
/label= Mature protein
                                                                                                                                                                                                                                                                                                                                                       1. .23
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                           ABB75954 standard; protein; 256 AA
                                                                                                                                                                                                                                                                   Cytokine; receptor; 4-1BB; mouse
                                                                                                                                                                                                                                  Murine cytokine receptor 4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00060843.
94US-00236918.
97US-00910449.
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                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
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                                          ckreceirkes 115
         CRPGQELTKQG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP
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06-MAY-1994;
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ADC25939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated and purified cDNA designated L25G25B encoding the mouse lymphokine macrophage inflammatory protein 1 alpha which can be used for modulating early myeloid progenitor cell differentiation.
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                                                           Score 62; DB 2; Length 256;
Pred. No. 0.0074;
Mismatches 0; Indels
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/note= "Mature receptor 4-1BB protein"
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138. 140
/note= "Asn is N-glycosylated"
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                                                               100.0%; Sc.
100.0%; Pri
tive 0;
                                                                                                                                                                                                                                                                                                                                                            Mouse receptore 4-1BB protein.
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                                                              Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                   1 CRPGQELTKQG 11
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N-PSDB; AAD35694.
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Best Local Similarity
Matches 11; Conserv
                                Sequence 256 AA;
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the invention
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                                                                                                                                                                       105
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Peptide
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01-FEB-1993;
05-JUN-1995;
22-OCT-1997;
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                                                         01-MAY-2003
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                                                                                                                                                                                      Kwon BS;
                Mus sp.
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                                                                                    receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; H4-1BB ligand binding blocker; mouse; receptor protein; H4-1BB; B-cell proliferation stimulator; T-cell proliferation enhancer; immune system supressor; transplantation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                          New cDNA gene encoding receptor protein 4-1BB, useful for isolating similar DNA sequences, and the encoded polypeptide and an antibody to it useful for identifying ligands, and for modulating immune cell activity.
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ADC25939 standard; protein; 256 AA
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                                                               Murine receptor 4-1BB protein.
                                                                                                                                                                                                       88US-00267577.
92US-00922996.
93US-00012269.
                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 2; 77pp; English.
                                                                                                                                                                                 04-FEB-2002; 2002US-00067122.
                                          (first entry)
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                                                                                               cancer; murine; mouse.
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es 11; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 256 AA;
                                          18-DEC-2003
                                                                                                                    Mus musculus
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30-JUL-1992;
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Matches
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The invention describes a cDNA, which encodes for human receptor protein H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein H4-1BB, or its fragments or derivatives, is useful as a probe for identifying ligands to the receptor protein H4-1BB, or for stimulating the proliferation of B-cells expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are useful for enhancing T-cell proliferation of activation. The cDNA or receptor protein H4-1BB is also useful for blocking H4-1BB ligand binding, which is particularly useful for suppressing the immune system during transplantation, or for treating autoimmune diseases. This is the amino acid sequence of mouse receptor H4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cDNA, or its encoded receptor protein H4-1BB, useful as probes to isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking H4-1BB ligand binding to facilitate organ transplantation or treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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92US-00922996.
93US-00012269.
95US-00460976.
97US-00955573.
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                                                                                                                                           2002US-00170997
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Best Local Similarity
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US2003082157-A1.
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The invention relates to a novel cDNA gene encoding receptor protein 4-1BB. The cDNA gene of the invention demonstrates immunostimulant activities and may be useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein encoded by the DNA. The protein, its fragments and derivatives may be useful as a probe to isolate ligands to receptor protein 4-1BB, for stimulating proliferation of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand binding. The antibody may be useful for enhancing T-cell proliferation or activation. Finally, the invention may be useful with respect to cancer research. The current sequence is that of the murine receptor 4-1BB peptide of the invention which contains residues 105-115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New receptor inducible by lymphocyte activation - used to develop prods. for the diagnosis and treatment of inflammatory host defence pathology.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILA; receptor inducible by lymphocyte activation; disease diagnosis; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "protein-kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "casein-kinase-II phosphorylation
                                                                                                                                                                                                                       Score 57; DB 7; Length 12;
Pred. No. 0.0026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "potential N-glycosylation site"
187. :213
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241. .244
/note= "potential ligand binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human receptor induced by lymphocyte activtion (ILA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..17
note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       AAR74087 standard; protein; 255 AA.
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                                                                                                                                                                                                                            91.9%;
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                          1 CRPGQELTKQG 11
                                                                                                                                                                                                                                                                                                                         1 CRPGQELTKSG
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N-PSDB; AAR74087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                               Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                        RESULT 1:
AAR74087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cDNA gene encoding receptor protein 4-1BB, useful for isolating similar DNA sequences, and the encoded polypeptide and an antibody to it, useful for identifying ligands, and for modulating immune cell activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulant; B-cell activation; T-cell proliferation;
                                                                                                                                                                                                                                                           The invention relates to an isolated and purified cDNA containing mouse lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by which the immune cells communicate with each other. Lymphokines are used therapeutically against immunologic diseases. Mouse lymphokine MIP-alpha can be used to modulate early myeloid progenitor cell differentiation. The present sequence is mouse lymphokine receptor 4-1BB peptide
                                                                                                                                                                    New isolated and purified cDNA designated L25G25B encoding the mouse lymphokine macrophage inflammatory protein 1 alpha which can be used for modulating early myeloid progenitor cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine receptor 4-1BB peptide containing residues 105-115.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 5; Length 12;
Pred. No. 0.0026;
0; Mismatches 1; Indels
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                                                                         (ADRE-) ADVANCED RES & TECHNOLOGY INC.
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                                                                                                                                                                                                                                   Disclosure, Col 53; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC25944 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88US-00267577.
92US-00922996.
93US-00012269.
                                                                                                                                                                                                                                                                                                                                                                                                                      91.9%;
90.9%;
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               92US-00922996
                                               88US-00267577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRPGQELTKSG 11
                                                                                                          Kwon BS, Broxmeyer HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; murine; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-678138/64.
                                                                                                                                        WPI; 2002-370577/40.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor 4-1BB;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1988;
30-JUL-1992;
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                30-JUL-1992;
                                               07-NOV-1988;
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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2. The TR2 gene is located on chromosome I at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists, antagonists and antibodies exhibit cytostatic, dermatological, antianaemic, immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
                                             ILA may be used to identify a host defence inflammatory response in body tissue. The ILA agents can be used to detect an ILA-mediated pathology such as atherosclerosis, autoimmune disease (rheumatoid arthritis, transplant rejection, pathogenic host defense responses to microorganism and mlignancy such as lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor-receptor related protein; TR2; human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.
                                                                                                                                                                                  80.6%; Score 50; DB 2; Length 255;
81.8%; Pred. No. 1.1;
                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      AAY94714 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 16; 373pp; English.
                Claim 55; Page 61; 91pp; English.
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99US-0126522P.
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99US-0147383P
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                  106 chodobbrkke 116
                                                                                                                                                                                                                                                   1 CRPGQELTKQG 11
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                                                                                                                                                                                                   Local Similarity
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GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA,
                                                                                                                                                  Sequence 255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1999;
26-MAR-1999;
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                                                                                                                                                                               Query Match
Best Local S:
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ni J,
                                                                                                                                                                                                                                                                                                                                    RESULT 16
AAY94714
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antinflammatory, neuroprotective, nootropic, antiparkinsonian, and cerebroprotective activity. The methods are useful for treating arthritis or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an autations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune haemolytic anaemia, dermatitis, allergic encephalomyelitis, rheumatorid arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency disorders (such as severely combined immunodeficiency with Igs). TR2, TR2-SV1 and/or TR2-SV2 polymucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancerous cells or inhibit the growth, progression and/or metastasis of cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, or Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human 4-1BB protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxic shock; tumour necrosis factor; TNF ligand; T-cell activation; inflammation; tumour prevention; viral infection; autoimmune disease; cellular proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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note= "putative signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19. .219 // note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW31759 standard; protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel human h4-1BBSV receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US003587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRPGQELTKQG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 CKQGQELTKKG 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1997.
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Claim 1a; Fig 1A-B; 28pp; English.

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The present sequence represents a novel human h4-1BBSV receptor. This is the tumour necrosis factor (TNF) family of ligands. It is induced by T-cell activation. The h4-1BBSV receptor nucleic acid and protein can be used for diagnosis and therapy. In particular, agonists of h4-1BBSV receptor can be used to treat and/or prevent tumours, restenosis, cytotoxicity, bacterial and viral infection, deleterious effects of ionising radiation, autoimmune disease, AIDS and graft-host rejection, to regulate immune responses, wound healing and cellular proliferation. Antagonists can be used to treat and/or prevent endotoxic shock, inflammation, cerebral malaria, activation of the HIV virus, graft rejection, bone resorption and cachexia
                                                                          Human 4-1BB receptor splicing variant and related DNA - used to develop products for treating e.g. tumours, viral infection, endotoxic chock, autoimmune disease or bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h4-1BBSV receptor; human; splice variant; antagonist; treatment; disease prevention; endotoxic shock; inflammation; cerebral malaria; HIV virus activation; graft rejection; bone resorption; cachexia;
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Pred. No. 3.2;
2; Mismatches 1; Indels
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/label= signal_peptide
19. .219
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                                                                                                                                                                                                    Claim 15; Fig 1; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.8%;
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Best Local Similarity 72..
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CKQGQELTKKG
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N-PSDB; AAX02162.
WPI; 1997-470806/43.
N-PSDB; AAT88969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 219 AA;
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                                This sequence represents a novel human h4-1BBSV receptor protein which is used in a method for making a human 4-1BB receptor splice variant which acts as an antagonist. The antagonist polypeptides may be used to treat/prevent disease states mediated by h4-1BBSV receptors such as endotoxic shock, inflammation, cerebral malaria, activation of the HIV virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding sequences are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding human 4-1BB receptor splicing variant - useful in treating h4-1BBSV mediated disease states such as endotoxic shock, inflammation, graft rejection and inactivation of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
33. 34
/note= "Site of deletion of residues GTFCDNNRNQICSPC
PPNSFSSAGGQRTCDICRQCK corresponding to amino acid
residues 34-69 of the wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h4-1BBSV receptor; human; splice variant; antagonist; treatment; disease prevention; endotoxic shock; inflammation; cerebral malaria; HIV virus activation; graft rejection; bone resorption; cachexia;
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                                                                                                                                                                                               Length 219;
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                                                                                                                                                                                             75.8%; Score 47; DB 2; 72.7%; Pred. No. 3.2; ive 2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                         AAW92524 standard; protein; 219 AA.
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70 CKQGQELTKKG 80
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Matches 8; Conserv
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                                                                                                                                                                     Sequence 219
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New nucleic acid encoding human 4-1BB receptor splicing variant - useful in treating h4-1BBSV mediated disease states such as endotoxic shock, inflammation, graft rejection and inactivation of HIV.

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(HUMA-) HUMAN GENOME SCI INC
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les 8; Conserv
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22-FEB-1999;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour; tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock; wound healing; autoimmune disease; acquired immunedeficiency syndrome; AIDS; graft-host rejection; cellular proliferation; cerebral malaria; bone resorption; human immunodeficiency virus; HIV; graft rejection; inflammation; antibacterial; immunosuppressive; vulnerary; vasotropic; antihlammatory; protozoacide; cachexia; immunomodulator; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to an isolated human 4-1BB receptor splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
                                                                                                                Gaps
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                                                                          Length 219;
                                                                                                               1; Indels
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/label= Mature_human_h4-1BBSV_receptor
                                                                                                                                                                                                                                                                                                                                                                                       Human h4-1BB splicing variant (h4-1BBSV) receptor.
                                                                         Score 47; DB 2;
Pred. No. 3.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Extracellular domain
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/label= Transmembrane_domain
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|abel= Signal_peptide
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97US-00816605.
99US-00253549.
                                                                       75.8%;
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                                                     Query Match
Best Local Similarity 72.,
8; Conservative
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represented in Fig 2
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N-PSDB; AAD15246.
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DILLON P J.
                                      Sequence 219 AA;
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13-MAR-1997;
22-FEB-1999;
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(YUGG/)
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AAE08545
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AC AAE08
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gene therapy. h4-1BBSV is useful for research, biological, clinical and therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives are useful as an immunogen to produce antibodies which are useful for isolating and identifying clones expressing the polypeptide or to purify the polypeptide. h4-1BBSV is useful for diagnosis and treatment of disorders of cells, tissues and organisms and its nucleic acid is useful for detecting complementary polynucleotides for e.g. as a diagnostic reagent and for chromosomal identification. h4-1BBSV receptor agonists are useful for preventing, treating tumours, restenosis, cytotoxicity, are useful for preventing, treating tumours, restenosis, cytotoxicity, and siseases, acquired immunodeficiency syndrome (ALDS) and graft-host rejection, to regulate immune responses, wound healing and cellular proliferation and antagonists are useful for treating and/or preventing endotoxic shock, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV) virus, bone resorption, graft rejection and cachexia. The present sequence is human h4-1BBSV receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19. .219
/label= h4-1BBSV_receptor.
/note= "region specifically claimed in claim 1b"
19. .150
/label= soluble_extracellular_domain
/note= "region specifically claimed in claim 1a"
151. .177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.8%; Score 47; DB 4; Length 219; ilarity 72.7%; Pred. No. 3.2; Conservative 2; Mismatches 1; Indels
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/label= transmembrane_domain
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'label= leader_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB84639 standard; protein; 219 AA.
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99US-00253549.
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Gaps

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Novel cDNA encoding human receptor protein H4-1BB - useful to produce the protein which is used to treat auto:immune disease and facilitate organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using probes based on the mouse receptor protein 4-1BB gene. The PCR product was used to screen a cDNA library of activated human T-cells. The isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct
                                                                                  The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423) are useful in a pharmaceutical composition for stimulating the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring mechanisms of T-cell activation, as they are expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It may also be used to stimulate proliferation of activated T-cells, used in therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H4-1BB; receptor protein; immunosuppressive; autoimmune disease; organ transplantation; cell membrane ligand.
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                                                                                                                                                                                                                                                                                   75.8%; Score 47; DB 2; Length 255; 72.7%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                           Claim 39; Page 47-48; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR70977 standard; protein; 255 AA.
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               106 ČKQGÓELTKKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H4-1BB receptor protein.
                                                                                                                                                                                                                                                                                                                                                            1 CRPGOELTKOG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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N-PSDB; AAQ86126.
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Best Local Similarity
        Cytokine, 4-1BB lig
to transduce signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplantation.
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                                                                                                                                                                                                                                                        Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1993;
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16-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kwon BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
AAR70977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                 This invention describes a novel human h4-1BBSV receptor or a sequence that is at least 85% identical to the h4-1BBSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, antiinflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome a disease related to underexpression of h4-1BBSV or for identifying agonists and antagonists. The soluble extracellular domain of h4-1BBSV receptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV), graft-host rejection, bone resorption or cachexia, tumours, autoimmune disease, ionizing radiation, acquired immunodeficiency syndrome (AIDS), for providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells and certain haematopoietic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.

This sequence represents the human 4-1BBSV receptor described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                 Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors, providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell; lymphocyte; activation; tissue culture; clone; cell lines; proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.8%; Score 47; DB (72.7%; Pred. No. 3.2; ive 2; Mismatches
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                                    Dillon PJ;
                                                                                                                                                                                           Example 2; Fig 1A-B; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US005036
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: ||||||:|
| CKQGQELTKKG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRPGQELTKQG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 4-1BB polypeptide
                                    Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-022265/03.
N-PSDB; AAQ75424.
                                                                     2003-066900/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 219 AA;
                                                                                       N-PSDB; ABS57520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1994;
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                                    Yu G,
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08-AUG-1995
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                                    Ni J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function as an accessory signaling molecule during T-cell activation and proliferation. Its amino acid sequence was deduced from a cDNA clone (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-1BB can be produced in transfected host cells. It is used to isolate receptor ligands, to stimulate B-cells expressing such ligands and to block H4-1BB ligand binding. A fusion protein of H4-1BB with human placental alkaline phosphatase can be used to modify immune responses. A monoclonal antibody raised against an immunoepitope (see also AAW04172) of H4-1BB is useful in the treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody specific for human receptor protein 4-1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating auto:immune diseases.
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human receptor protein H4-1BB (AAW04174) has the potential to
                                                                                                                                                                                                                                           Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell; B-lymphocye; B-cell; immunostimulant; cancer; autoimmune disease; graft rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.8%; Score 47; DB 2; Length 255; 72.7%; Pred. No. 3.7; vative 2; Mismatches 1; Indels
   1; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 36-37; 48pp; English
                                                                                                                            AAW04174 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                       96WO-US003965
                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00409851
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8; Conservative
                                                       106 CKOGOELTKKG 116
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                                                                                                                                                                                                                Human receptor H4-1BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-443138/44.
N-PSDB; AAT39546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kwon BS, Kang C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 255 AA;
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                            WO9629348-A1
                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1996;
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                                                                                                                                                                                   12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                        26-SEP-1996
                                                                                                                                                       AAW04174;
Matches
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AAW26658
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AAW26658 standard; protein; 255 AA

(revised)

25-MAR-2003

AAW26658

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools.
                                                   4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell; proliferation; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2; Length 255; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                        /label= Cytoplasmic
/label= Cytoplasmic
/lote= "Asn is N-glycosylated"
/note= "Asn is N-glycosylated"
/note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                              214. .255
/label= Extracellular
                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                 1. .23
/label=_Sig_peptide
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Col 43-44; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY28688 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                          94US-00236918.
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  (first entry)
                                                                                                                                                                                                                                      187. .213
/label= Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodwin RG,
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRPGOELTKOG 11
                            Human 4-1BB receptor.
                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-502333/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT91026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 255 AA;
                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                    Alderson MR,
 25-FEB-1998
                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        06-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1993;
                                                                                                                                                                                                                                                                                                     US5674704-A.
                                                                                                                                                                                                                                                                                                                             07-OCT-1997
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                                                                                                                                Peptide
                                                                                                                                                           Domain
                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                Domain
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AAY28688
ID AAY280
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AC AAY280
XX
DT 13-OCT
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This invention describes a novel use of the human monocyte growth factor CC CD137, or its functional analogs, for (i) stimulating proliferation of peripheral monocytes; and (ii) treating diseases that are associated with disorders of a cellular system that includes monocytes (and/or their disorders of a cellular system that includes monocytes (and/or their cc derived cells, precursor or progenitors) or where the origin and/or products of the invention have antitumor, antibacterial, and/or cells invention have antitumor, antibacterial, antiviral, antifungal and immunostimulatory activity. Stimulating proliferation of antifungal and inmunostimulatory activity. Stimulating proliferation of complexes and damaged cells, and improves antibody (in) dependent complexes and damaged cells, and improves antibody (in) dependent cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat diseases associated with a defective immune response where caused by indequate numbers of active monocytes/macrophages, especially damage to the hematopoietic system (leucopenia) caused by chemotherapy or radiation therapy; disorders of wound healing (e.g. in dialysis or diabetic fungal or viral infections; (non-)congenital or (non-)inherited diseases or injury to the immune system; injury induced by treatment with immunosuppressants (e.g. patients with chronic venous insufficiency); tumors, bacterial, consultant, in gene therapy procedures. Proliferation of peripheral monocytes is achieved independently of hematopoietic stem cells. This enterior sequence represents the human CD137 protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of monocyte growth factor CD137 for stimulating proliferation of peripheral monocytes, particularly for treating immune deficiency, e.g. following cancer therapy.
bacterial; viral infection; immunosuppressant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 1A; 57pp; German.
                                                                                                                                                                                              99WO-EP001440.
                                                                                                                                                                                                                                        98EP-00103859.
                                                                                                                                                                                                                                                                                                                                    Schwarz H, Langstein J;
                                                                                                                                                                                                                                                                                        (MERC ) MERCKLE GMBH
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-550983/46.
N-PSDB; AAZ09769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 255 AA;
                                                                                                                                                                                              05-MAR-1999;
                                                                                                                                                                                                                                          05-MAR-1998;
                                                         Homo sapiens
                                                                                                                                                 10-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a human receptor protein 4-1BB. 4-1BB is structurally related to members of the nerve growth factor receptor. It contains a putative zinc finger structure similar to that of yeast e1F-2b protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation; B cell proliferation; treating cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand binding has practical application in the suppression of immune system during organ transplantation or against autoimmune diseases including diabetes, rheumatoid arthritis, and lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD137; monocyte growth factor; proliferation; peripheral monocyte; treatment; disease; antitumor; antibacterial; antiviral; antifungal; immunostimulatory; non-specific immune response; phagocytosis; intracellular destruction; microorganism; immune complex; antibody; cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia; chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                     Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation; mouse 4-1BB cDNA; monoclonal antibody; immune response; organ transplantation; autoimmune disease; diabetes; cancerous tumour; rheumatoid arthritis; lupus; nerve growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
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                                                                                                                                                                                                                        Location/Qualifiers
18. .255
/note= "Purified human 4-1BB"
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                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US000823.
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                 Human receptor protein 4-1BB
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-1999;
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                                                                                                                                                                                  Homo sapiens
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AAY33214
ID AAY3
XX
AC AAY3
XX
DT 18-1
XX
DE HUME
XX
KW CD1:
KW tree
KW imm
KW cyte
KW chee
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Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
                                                        Gaps
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0
Query Match
75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                            106 CKQGQELTKKG 116
                                                                                                              1 CRPGOELTKOG 11
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nootropic;

Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.

Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.

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New human 4-1BB receptor splicing variant polypeptides and polynucleotides, useful for research, diagnosis, prevention and treatment of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock; wound healing; autoimmune disease; acquired immunedeficiency syndrome; AIDS; graft-host rejection; cellular proliferation; cerebral malaria; bone resorption; human immunodeficiency virus; HIV; graft rejection; inflammation; antibacterial; immunosuppressive; vulnerary; vasotropic; antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47;
                                                                                                                                                                                                                                                             Dillon PJ
                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 2; 28pp; English.
                                                                                                                                                             96US-0013474P.
97US-00816605.
99US-00253549.
                                                                                                                                                                                                                                                                                                                                       syndrome and graft rejection.
                                                                                                                                        19-DEC-2000; 2000US-00739394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.8%;
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                                                                                                                                                                                                                                       DILLON P J.
                                                                                                                                                                                                                                                                                WPI; 2001-529104/58
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Best Local Similarity
Matches 8; Conserv
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YU G.
GENTZ R.
                                                                                                US2001014465-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 255 AA;
                                                                          Homo sapiens.
                                                                                                                                                                                                                                                             Yu G,
                                                                                                                                                             15-MAR-1996;
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22-FEB-1999;
                                                                                                                    16-AUG-2001
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                                                                                                                                                                                                       (NIJJ/) 1
(YUGG/) 7
(GENT/) (
                                                                                                                                                                                                                                       (DILL/)
                                                                                                                                                                                                                                                             Ni J,
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Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.

Disclosure; Fig 2; 285pp; English.

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N 1

Gentz RL,

Ruben SM,

Wei Y,

WPI; 2001-041051/05.

(HUMA-) HUMAN GENOME SCI INC

18-MAY-2000; 2000WO-US013515.

20-MAY-1999;

WO200071150-A1.

30-NOV-2000

Homo sapiens

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The present invention relates to an isolated human 4-1BB receptor
splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in
gene therapy. h4-1BBSV is useful for research, biological, clinical and
therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives
are useful as an immunogen to produce antibodies which are useful for
isolating and identifying clones expressing the polypeptide or to purify
the polypeptide. h4-1BBSV is useful for diagnosis and treatment of
disorders of cells, tissues and organisms and its nucleic acid is useful
for detecting complementary polynucleotides for e.g. as a diagnostic
reagent and for chromosomal identification. h4-1BBSV receptor agonists
are useful for preventing, treating tumours, restenosis, cytotoxicity,
care useful for preventing, treating tumours, estenosis, cytotoxicity,
autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-
host rejection, to regulate immune responses, wound healing and cellular
proliferation and antagonists are useful for treating and/or preventing
endotoxic shock, inflammation, cerebral malaria, activation of human
immunodeficiency virus (HIV) virus, bone resorption, graft rejection and
cachexia. The present sequence is human h4-1BB receptor
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AAB50521 standard; protein; 255 AA

(first entry)

15-MAR-2001

AAB50521;

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The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor (TNFR-5 or TRS)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial colls and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polymeptides are useful for treating and/or preventing diseases are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune diseases associated with increased or decreased apoptotic cell death. The TRID colymucleotides, proteins, antibodies, agonists and antagonists are useful in the disorders; (c) diseases associated with increased apoptotic autoimmune disorders; (c) with an advisable or decreased apoptotic or the present or decreased autoimmune disorders; (c) diseases associated with increased apoptotic autoimmune disorders; (d) wirelighted with increased apoptotic or decreased apoptotic or decreased apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disorders; and (e) viral infection. The present sence represents a tumour necrosis factor receptor used in comparison
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB75955 standard; protein; 255 AA.
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Best Local Similarity
Matches 8; Conserv
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ABB75955
ID ABB759
XX
AC ABB759
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The invention relates to an agonist or antagonist of MOCEPTIN (a member of the Tumour Necrosis Factor Receptor family) activity. The antagonist of the Tumour Necrosis Factor Receptor family) activity. The antagonist or agonist or antagonist, is useful for preventing or treating an obesity-related disorder or disease in an individual. In particular, the agonist of MOCEPTIN activity is useful for treating or preventing obesity-related diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance, clabetes, stroke or hypertension. The agonist is also useful for reducing body mass, or for treating or preventing disorders associated with excessive weight loss, e.g. cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease-related weight loss, or anorexia. The present inflammatory disease-related weight loss, or anorexia. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis Factor Receptor family) activity, useful for preventing or treating obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing body mass.
                                                                                                                                                                                                                                                                 MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic; antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective; hypotensive; immunomodulator; antidepressant; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .17
/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18. .255
/note= "mature protein"
18. .186
/note= "extracellular domain"
187. .213
/note= "transmembrane domain"
214. .255
/note= "intracellular domain"
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Pred. No. 3.7;
2; Mismatches 1
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                                                  ABR39863 standard; protein; 255 AA
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Best Local Similarity 72.7%;
Matches 8; Conservative ;
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                                                                                                                                                                                                                   Human MOCEPTIN polypeptide
                                                                                                                                                               (first entry)
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N-PSDB; ACC47324.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                 11-AUG-2003
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                                                                                                             ABR39863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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RESULT 31
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ID ABR39
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AC ABR39
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AC ABR39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the protein sequence of the human cytokine receptor, 4-1BB. The sequence was deduced from a cDNA clone (see ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion of the extracellular (ligand binding) domain of the human 4-1BB cytokine receptor was utilised in a human 4-1BB ligand (4-1BB-L, see which was used to identify the human 4-1BB ligand (4-1BB-L, see polypeptides and human 4-1BB polypeptides, as well as DNA sequences encoding them, recombinant expression vectors and host cells, and methods for producing the novel polypeptides by cultivating the transformed host cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from their extracellular domains, have therapeutic value. Antibodies that are immunoreactive with 4-1BB-L or human 4-1BB are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 3.7;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                   / 1abel= Mature_protein
24. .186
/note= "extracellular domain"
138. .140
/note= "Asn is N-glycosylated"
149. .151
/note= "han is N-glycosylated"
186. .213
/note= "transmembrane region"
214. .255
/note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                     1. .23
/label=_Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Col 43-44; 31pp; English.
                                                                                                                                                                                                                                                     socation/Qualifiers
                                                                                                                                                 Cytokine; receptor; 4-1BB; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00060843.
94US-00236918.
97US-00910449.
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                                                                                           Human cytokine receptor 4-1BB.
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                                    12-JUL-2002 (first entry)
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-380940/41.
N-PSDB; ABL54048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-1993;
06-MAY-1994;
05-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                            Protein
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Gaps .; 0 Length 255 Indels

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CRPGQELTKQG 11 |: ||||||:|

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106 CKQGQELTKKG 116

106 CKQGQELTKKG 116

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Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive; anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator; vasotropic; gene therapy; chromosome mapping; extracellular domain; endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease; human immunodeficiency virus; HIV; graft-host rejection; bone resorption; cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome; AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis; autoimmune disease; h4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.8%; Score 47; DB 6; Length 255; ilarity 72.7%; Pred. No. 3.7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                ABB84640 standard; protein; 255 AA.
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97US-00816605.
99US-00253549.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2000; 2000US-00739394
                                                                                                                                                      (first entry)
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                                                                                                                                                                                                            Human h4-1BB receptor
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Best Local Similarity
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                                                                                                                                                      05-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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22-FEB-1999;
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                                                                                           ABB84640;
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ABB84640

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RESULT 34
ADC78803
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                                                                                                                                                                                                                                                                                                                       This invention describes a novel human h4-1BBSV receptor or a sequence that is at least 85% identical to the h4-1BBSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, antinflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome adisease related to underexpression of h4-1BBSV or for identifying adisease related to underexpression of h4-1BBSV or for identifying adisease related to underexpression of h4-1BBSV or for identifying adjonists and antagonists. The soluble extracellular domain of h4-1BBSV receptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV), graft-host rejection, bone resorption or cachexia, tumours, autoimmune disease, ionizing resistance to bacteria, immunodeficiency syndrome (AIDS), for providing resistance to bacteria, certain haematopoletic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist. This sequence represents the human 4-1BB receptor described in the
Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors, providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis.
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01-JAN-2004 (first entry)

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Gaps

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The invention relates to a method and apparatus for applying adhesive to packaging in a variety of configurations. The method involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction. The invention is useful for e.g. soap boxes, cereal boxes, bottle carriers, can boxes. The present sequence is human protein. Note: There is no specific information about the sequence in the
                                                                                                                                                                                                                                                                                                                                                                                                                                            Paper board container manufacture for soap boxes, involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                           /note= "Encoded by AGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 12-13; 46pp; English.
                                                                                                                                                                 Location/Qualifiers
AAE39531 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC78803 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                            08-JUN-2001; 2001US-00877336.
                                                                                                                                                                                                                                                                                                        08-JUN-2001; 2001US-00877336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.8%; 72.7%;
                                                                                Human protein SEQ ID NO: 2.
                                                                                                           Human; adhesive; packaging
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 ČKQĞQELTKKG 116
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                                                                                                                                                                                                                                                                                                                                                                          Walsh JC, Hawkins KE;
                                                                                                                                                                                                                                                                                                                                 (WALS/) WALSH J C.
(HAWK/) HAWKINS K E.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-266968/26.
N-PSDB; AAD59981.
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                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 255 AA;
                                                                                                                                                                                                                     US2003000851-A1
                                                                                                                                        Homo sapiens,
                                                     18-DEC-2003
                                                                                                                                                                                                                                                  02-JAN-2003
                           AAE39531;
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RESULT 36
ADE87541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences of human PRO
                                                                                                                                                                                                                                                                                                                                      New PRO polynucleotide and polypeptide, useful for the manufacture of a medicament for diagnosing or treating cancer or inflammatory bowel disorder e.g., ulcerative colitis or Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of human proteins. The DNA and protein sequences of the invention are useful futhe diagnosis and treatment of cancer and inflammatory bowel disease (e.g. ulcerative colitis or Crohn's disease). The present amino acid sequence represents a human PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain-immunoglobulin fusion protein-associated protein #77.
                       human; PRO; cancer; inflammatory bowel disease; ulcerative colitis; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 7; Length 255; Pred. No. 3.7; 1; Indels 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; SEQ ID NO 32; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD25599 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001US-0367358P.
                                                                                                                                                                   15-OCT-2002; 2002WO-US033070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2002; 2002US-00207655.
                                                                                                                                                                                                 19-OCT-2001; 2001US-0340083P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 ČKQGQELTKKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRPGOBLIKOG 11
                                                                                                                                                                                                                                                              Goddard A, Gurney AL;
                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
Human PRO protein #16
                                                                                                                                                                                                                                                                                            WPI; 2003-481990/45.
                                                                                                                                                                                                                                                                                                           N-PSDB; ADC78802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 255 AA;
                                                                                                     WO2003034984-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003118592-A1
                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004
                                                                                                                                     01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD25599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
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comprising a binding domain polypeptide that is fused to an immunoglobulin have no comprising a binding domain polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide constant region polypeptide control in manupolobulin hinge region polypeptide. The fused for the first constant region polypeptide control in hinge region polypeptide derived from (a) having 30 rm core cysteine residues, hinge region polypeptide, derived from (a) having 30 rm core cysteine residues, where the first cysteine residues, where the first cysteine is not mutated, contains 2 cysteine residues, where the first cysteine is not mutated, and a mataced human igd1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine residues, in a mataced human igd1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region protein is capable of a least one immunoglobulin hinge region protein contains no cysteine residues. The binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the bolymetected with a recombinant expression antignant contains of an expected of having a malignant condition or a promoter. The binding domain-immunoglobulin fusion protein and carrier, and treating a subject fusion protein or polymulation conquesting the binding domain-immunoglobulin fusion protein is useful for treating a construct, producing the binding domain-immunoglobulin fusion protein and a carrier, and treating domain-immunoglobulin fusion protein and a carrier and the polymulation of a binding domain-immunoglobulin fusion prote
                                                                                                                                                                                                                                                                                                                                                              New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                      Hayden-Ledbetter MS, Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 160; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE87541 standard; protein; 255 AA.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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                                                                                                                         (GENE-) GENECRAFT INC.
                                                                                                                                                                                                                                                                                         WPI; 2003-801317/75.
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Best Local Similarity
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The invention describes a cDNA, which encodes for human receptor protein H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe to isolate DNA sequences encoding for proteins similar to the receptor protein H4-1BB, or its fragments or derivatives, is useful as a probe for identifying ligands to the receptor protein H4-1BB, or for stimulating the proliferation of B-cells expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are useful for enhancing T-cell proliferation of activation. The cDNA or receptor protein H4-1BB is also useful for blocking H4-1BB ligand binding, which is particularly useful for suppressing the immune system during transplantation, or for treating autoimmune diseases. This is the amino acid sequence of unknown human receptor H4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                        immunosuppressive; H4-1BB ligand binding blocker; human;
receptor protein; H4-1BB; B-cell proliferation stimulator;
T-cell proliferation enhancer; immune system supressor; transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s probes to
for blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; LP protein; cell proliferative disorder; actinic keratinosis;
arteriosclerosis; psoriasis; leukaemia; lymphoma; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cDNA, or its encoded receptor protein H4-1BB, useful as probes isolate DNAs or ligands to the receptor protein H4-1BB, or for bloo H4-1BB ligand binding to facilitate organ transplantation or treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human LP283 splice variant protein, LP346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29933 standard; protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2,
                               Umknown human receptor H4-1BB,
                                                                                                                                                                                                                                                                         92US-00922996.
93US-00012269.
95US-00460976.
97US-00955573.
                                                                                                                                                                                                                               2002US-00170997
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72.7%;
 (first entry)
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Best Local Similarity 72.7
Matches 8; Conservative
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CKQGQELTKKG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-576599/54.
                                                                                                          autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADE87540.
                                                                                                                                                                  US2003082157-A1
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                                                                                                                                                                                                                                                                          30-JUL-1992;
01-FEB-1993;
05-JUN-1995;
22-OCT-1997;
                                                                                                                                                                                                                              12-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                    (KWON/) KWON
                                                                                                                                      Homo sapiens
  29-JAN-2004
                                                                                                                                                                                                                                                           07-NOV-1988;
                                                                                                                                                                                                01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                 Kwon BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 37
8
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The present invention relates to LP (LP318a, LP318b, LP288, LP289, LP343, LP319a, LP319b, LP319b, LP317, LP283, LP344, LP345 or LP346) proteins and LP319a, LP319b, LP321, LP317, LP283, LP344, LP345 or LP346) proteins and collaboration are polynucleotides encoding such proteins. Sequences of the invention are used to diagnose, treat or prevent cell proliferative disorders (e.g. actinic keratinosis, arteriosclerosis, psoriasis, leukaemia, lymphoma, actinic keratinosis, arteriosclerosis, autoimmune or inflammatory disorders (e.g. AIDS (acquired immune deficiency syndrome), Addison's disease, albergies, ankylosing spondylitis, amyloidosis, anaemia, asthma, acton, s disease, Goodpasture's syndrome, gout, Hashimoto's thyroiditis or Grave's disease, angina pectoris, myocardial infarction, atherosclerosis or hypertension), neurological disorders (e.g. stroke, Parkinson's disease or Alzheimer's disease) or developmental disorders (e.g. Down's syndrome or cerebral palsy). They are also used in gene therapy. The present sequence is human LP283 splice variant protein,
melanoma; cancer; inflammatory disorder; Addison's disease; allergy; acquired immune deficiency syndrome; AIDS; ankylosing spondylitis; amyloidosis; anaemia; asthma; Crohn's disease; Goodpasture's syndrome; gout; Grave's disease; Hashimoto's thyroiditis; cardiovascular disorder; congestive heart failure; ischaemic heart disease; myocardial infarction; angina pectoris; atherosclerosis; hypertension; neurological disorder; stroke; Parkinson's disease; Alzheimer's disease; developmental disorder; bown's syndrome; cerebral palsy; gene therapy; nephrotropic; nootropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mammalian LP polynucleotides and proteins, useful in gene therapy, e.g. for treating or preventing cancers, autoimmune (e.g. AIDS), cardiovascular (e.g. myocardial infarction) or neurological (e.g. stroke)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GP;
Seno F
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J, Rowlinson SW, Sankhavaram PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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9
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Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 286-287; 290pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02951 standard; protein; 389 AA.
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                                                                                                                                                                                                                                                                                                               16-MAR-2001; 2001US-0276596P.
13-APR-2001; 2001US-0283654P.
20-APR-2001; 2001US-0285238P.
03-MAY-2001; 2001US-0288548P.
11-MAY-2001; 2001US-0290351P.
                                                                                                                                                                                                                                                                                01-MAR-2002; 2002WO-US005093.
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88.9%;
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Perkins DR, Rosteck PRJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 88.9
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                                                                                                                                                                                                       WO200274906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR, Ro
Zhi Y;
                                                                                                                                                                                                                                             26-SEP-2002
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Su EW,
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(first entry)

12-SEP-2001

Human POLY6 protein sequence SEQ ID NO:12.

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granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                      Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
        Angiotensin converting enzyme (ACEV) splice variant protein #51
                                                                                                                                                                                                                                                                                                                                                                                     Levine Z, David A, Azar I, Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 51; 519pp; English
                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000WO-IL000766.
                                                                                                                                                                                                                                                                                                               17-NOV-1999; 99IL-00132978.
10-DEC-1999; 99IL-00133455.
                                                                                                                                                                                                                                                                                                                                                            (COMP-) COMPUGEN LID.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS06051.
                                                                                                                                                                                                                              WO200136632-A2
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                        25-MAY-2001
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The sequence represents an angiotensin converting enzyme splice variant of (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial

Sequence 389 AA;

Gaps ö 69.4%; Score 43; DB 4; Length 389; 72.7%; Pred. No. 30; 3; Indels; ive 0; Mismatches 3; Indels Query Match Best Local Similarity 72., Local Similarity 72., 8, Conservative

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8 셤

AAG68259 standard; protein; 845 AA AAG68259, RESULT 39 AAG68259 dxyxh

14-FEB-2002

Human; POLYX; gamma aminobutyric acid receptor; GABA receptor; epidermal growth factor; EGF; complement receptor; HSPC; syntaxin; haematopoietic stem and progenitor cell; sulphotransferase; prohibitin; antidepressant; cerebroprotective; antiparkinsonian; neotropic; relaxant; anticonvulsant; neuroleptic; neuroprotective; antialcoholic; cardiant; tranquilliser; antiarrhythmic; psychiatric; medical; depression; stroke; parkinson's disease; Huntington's disease; Tourette's syndrome; anxiety; amyotrophic lateral sclerosis; head trauma; Alzheimer's disease; alcoholism; vigilance; muscle tension; epileptogenic; memory function; cardiomyopathy; arrhythmogenic right ventricular dysplasia. 20-APR-2000; 2000US-0198645P. 26-APR-2000; 2000US-0199476P. 26-APR-2000; 2000US-0199880P. 26-APR-2000; 2000US-0200024P. 26-APR-2000; 2000US-0200025P. 09-UN-2000; 2000US-0210809P. 17-UUL-2000; 2000US-0218591P. 11-AUG-2000; 2001US-024610P. 09-FEB-2001; 2001US-0267673P. 27-FEB-2001; 2001US-0271814P. ; 2000US-0198293P. ; 2000US-0198645P. ; 2000US-0199476P. ; 2000US-0199880P. 19-APR-2001; 2001WO-US012854 WO200179294-A2. Homo sapiens. 25-OCT-2001

(CURA-) CURAGEN CORP.

Vernet CAM, Fernandes E, Shimkets RA, Majumder K; Colman SD, Zerhusen BD, Spytek KA, Burgess CE, Liu X; Taupier RJ, Padigaru M,

WPI; 2002-017601/02. N-PSDB; ABA03875. New isolated polypeptides for treating a broad range of pathological states, e.g., depression, stroke, Parkinson's disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma, and Alzheimer's.

Claim 1; Page 33-34; 155pp; English.

The present invention describes polypeptides (I), designated POLYX

CD polypeptides (e.g. POLY1.4 are members of the gamma aminobutyric acid

(II) encoding them. POLY1-4 are members of the gamma aminobutyric acid

(GABA) receptor family; POLY5-11 are members of the epidermal growth

CC factor (BGF) family; POLY3-11 are members of the complement receptor

CA family; POLY12 is a member of the haematopoietic stem and progenitor cell

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

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(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

(HSPC) family; POLY13 is a member of the cerebroyncective, antialcoholic, cardiant, tranquilliser and medicament for treating a syndrome as a therapeutic in the mammal, especially patients suffering from, e.g., pathological state in a mammal, especially patients suffering from, e.g., pathological state in a mammal, especially patients suffering from, e.g., psychiatric and medical conditions, depression, stroke, Parxinson's clesses, Huntington's disease, Tourette's syndrome, amyotrophic lateral scale anxiety, muscle tension, epileptogenic activity and memory functions, correctly muscle tension, epileptogenic activity and memory functions, correctly and arrhythmogenic right ventricular dysplasia. The

Sequence 845 AA;

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Gaps

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Gamma-aminobutyic acid receptor-like protein; depression; stroke; GABA receptor-like protein; Parkinson's disease; Huntington's disease; Tourette's syndrome; amyotrophic lateral sclerosis; head trauma; Alzheimer's disease; alcoholism; vigilance; anxiety; muscle tension; epileptogenic activity; memory; cardiomyopathy; cancer; angiogenesis; arrhythmogenic right ventricular dysplasia; renal disease; diabetes; Epidermal growth factor like protein; leukaemia; lupus; anaemia; ulcer; haematopoietic stem and progenitor cell like protein; cirrhosis; sulfotransferase-like protein; cholangitis; hepatitis; hyperthyroidism; developmental disorder; Syntaxin-like protein; myxoid liposarcoma; asthma; Lambert-Eaton myasthenic syndrome; acute myeloidleukaemia;
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    Length 845;
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  Score 43; DB 5;
Pred. No. 66;
0; Mismatches
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  69.4%;
88.9%;
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2000US-0199476P,
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2000US-0210809P.
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2000US-0224610P
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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MACDOUGALL J R.
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                                                                                                               1 CRPGQELTK 9
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11-AUG-2000;
27-FEB-2001;
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26-APR-2000;
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ABU12092
ID ABU12092
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The invention describes an isolated POLYX (POLY1-17) polypeptide and its variant. POLYX polypeptides (especially POLY5, POLY6 and POLY7), the polynucleotides encoding them (I) and an anti-POLYX-antibody (III) are

Claim 1; Page 20-21; 91pp; English.

Search completed: May 5, 2004, 14:38:04 Job time : 5.46233 secs

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cc useful for treating or preventing a pathology associated with POLYX clisease. POLYX polypeptide is also useful for identifying an agent that chinds to POLYX and a cell expressing POLYX is useful for identifying a cc binds to POLYX and a cell expressing POLYX is useful for identifying a cc therapeutic agent for use in treatment of a pathology related to aberrant cc expression or physiological interactions of the polypeptide. (III) is useful for treatment of POLYX in a sample. POLYI—4 (GABA receptor—like to proteins) are useful for the treatment of psychiatric and medical conditions, depresesion, stroke, Parkinson's disease, Huntington's conditions, appresession, stroke, Parkinson's disease, Huntington's conditions, depresession, amyotrophic lateral sclerosis, head trauma, altaheimer's disease, alcoholism, vigicalnee, anxiety, muscle tension, conditions and memory functions, cardiomyopathy and arrhythmogenic activity and memory functions, cardiomyopathy and arrhythmogenic right ventricular dysplasia. POLY5-8 (Epidermal growth factor like proteins) may be useful for treating carrant carnythmosensis, renal disease and diabetes. POLY12 (haematopoietic stem and grogenesis, renal disease and diabetes. POLY12 (haematopoietic stem and creating cirrhosis, cholangitis, hepatitis, ulcers, hyperthyroidism and developmental disorders. POLY1-16 (Syntaxin-like proteins) may be useful for treatment of Lambert-Eaton mysathenic syndrome, asthma, myxoid liposarcoma and acute myeloid leukaemia, and POLY 18 may be useful in treatment of Lambert-Eaton mysathenic syndrome, asthma, myxoid liposarcoma and acute myeloid leukaemia, and POLY 18 may be useful in treatment of Lambert-Eaton mysathenic syndrome, sethma, myxoid liposarcoma and caute myeloid leukaemia, and POLY 18 may be useful in treatment of Lambert-Eaton mysathenic syndrome, sethman myzotein and for identifying and/or ectivity of POLYX protein and for identifying and, or evaluating a novel human protein activity. This is the amino acid sequence of
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Pred. No. 66;
0; Mismatches 1; Indels
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Run on:

12, Appl 2, Appli 7, Appli 7, Appli 4, Appli 3, Appli 28279, A

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US-09-746-359A-59
US-09-746-359A-15
US-09-746-359A-15
US-09-746-359A-14
US-09-746-359A-57
US-09-548-130-6
US-09-548-130-6
US-09-548-130-6
US-09-511-423-2
US-08-911-423-2
US-09-512-363-7
US-09-176-200-7
US-09-286-529-4
US-09-252-991A-28279
US-09-358-383C-16
US-09-358-383C-16
US-09-461-325-481
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US-08-012-269A-13
US-08-012-269A-13
Sequence 13, Application US/08012269A
Patent No. 6362325
GENERAL INFORMATION:
TITLE OF INVENTION: WURINE 4-1BB GENE
FILE REFERENCE: 740.009US1
CURRENT APPLICATION NUMBER: US/08/012,269A
CURRENT FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: US 07/922,996
PRIOR FILING DATE: 1992-07-30
PRIOR FILING DATE: 1998-11-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 11
TYPE: PRT
CORGANISM: Mus musculus
US-08-012-269A-13
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US-08-974-022-52
; Sequence 52, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, Willaim J.
APPLICANT: Calcop, David L.
; APPLICANT: Calcop, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
; COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                May 5, 2004, 14:35:32 ; Search time 1.58219 Seconds (without alignments) 358.923 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-706-945B-139
US-08-776-945B-139
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US-08-236-918A-6
US-08-012-269A-2
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US-09-150-864A-8
US-09-150-864A-8
US-09-150-864A-8
US-09-150-864A-8
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US-09-150-86-11
US-09-150-864A-8
US-09-673-545A-2
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62
1 CRPGQELTKQG 11
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                             Query Match 100.0%; Score 62; DB 3; Length 191; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 11; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids

LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 52, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                               RESULT 4
US-08-795-447A-52
; Sequence 52, Application US/08795447A
; Patent No. 6284728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
                                                                                                                                                               105 ČŘPGQELTKOG 115
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linear
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MOLECULE TYPE: protein
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COUNTRY: USA
ZIP: 91362-1789
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US-08-974-186-52
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/08795445A; Sequence 52, Application US/08795445A; Patent No. 6284485; GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Clarg, David L.
APPLICANT: Clarg, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                    FILING CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 11; Conservative
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; MOLECULE TYPE: protein
US-08-974-022-52
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US-08-795-445A-52
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                                                                                                                                                                                                                                                                                                                                                                        / Sequence 139, Application US/08706945D
/ Sequence 139, Application US/08706945D
/ Patent No. 6369027
/ GENERAL INFORMATION:
/ APPLICANT: Boyle, William
/ APPLICANT: Lacey, David
/ APPLICANT: Calzone, Frank
/ APPLICANT: Calzone, Frank
/ APPLICANT: Chang, Ming-Shi
/ TITLE OF INVENTION: Osteoprotegerin
/ TITLE OF INVENTION: Osteoprotegerin
/ FILE REFERENCE: A-378CIP
/ CURRENT APPLICATION NUMBER: US/08/706,945D
/ CURRENT PILING DATE: 1996-09-03
/ PRIOR FILING DATE: 1995-12-22
/ NUMBER OF SEQ ID NOS: 145
/ SOFTWARE: Patentin version 3.1
/ LENGTH: 191
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Sequence 53, Application US/08577788C

Patent No. 6613544

GENERAL INFORMATION;

APPLICANT: Boyle, William

APPLICANT: Calzone, Frank

APPLICANT: Chang, Ming-Shi

TILLE OF INVENTION: Osteoprotegerin

FILE REFERENCE: A-378 Rev

CURRENT APPLICATION: Osteoprotegerin

FILE REFERENCE: A-378 Rev

CURRENT FILING DATE: 1995-12-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.1

LENGTH: 191
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                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-52
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  STRANDEDNESS: single
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; ORGANISM: Homo sapiens
US-08-706-945D-139
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CRGANISM: Mus musculus
US-08-577-788C-53
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Best Local Similarity
Matches 11; Conserva
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US-08-706-945D-139
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Sequence 52. Application US/0879546B

Patent No. 6288032

GENERAL INFORMATION:

APPLICANT: Boyle, Willaim J.

APPLICANT: Calzone, Frank J.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STRATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,446B
                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-186-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRPGOELTKOG 11
California
                                             91320-1789
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US-08-795-446B-52
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Sequence 3, Application US/09623545A;
Fatent No. 6627200;
Fatent No. 6627200;
Fatent No. 6627200;
Fatent No. 6627200;
Fatent No. 6627200;
FILE REFERENCHION: UTILIZATION OF PERIPHERAL MONOCYTES;
FILE REFERENCE: 30424.1USWO
CURRENT APPLICATION NUMBER: US/05/623,545A;
CURRENT FILING DATE: 2000-09-05;
FRIOR APPLICATION NUMBER: ED 98103859.9;
FRIOR FILING DATE: 1999-03-05;
FRIOR FILING DATE: 1999-03-05;
NUMBER OF SEQ ID NOS: 3;
SOFTWARE: PatentIN Ver. 2.1;
FALOR FILING NOS: 3;
FRIOR FILING DATE: 1000-03-05;
FRIOR FILING DATE: 1000-03-05;
FRIOR FILING DATE: 1000-03-05;
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FRIOR FILING DATE: 1000-03-05;
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FRIOR FILING
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                                                                                                                                                                                                                                                                Query Match 100.0%; Score 62; DB 4; Length 256; Best Local Similarity 100.0%; Pred. No. 0.0021; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
    TILL OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR PILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1998-11-07
; NUMBER OF SEQ 1D NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ 1D NO 2
; LENGTH: 256
                                                                                   ; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
US-09-150-864A-6
                 PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 CRPGOELTKOG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus
US-09-623-545A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
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           SOFTWARE: I
SEQ ID NO 6
LENGTH: 256
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// Sequence 6, Application US/09150864A

// Sequence 6, Application US/09150864A

// Patent No. 6355779

// GENERAL INFORMATION:

// APPLICANT: Alderson, Mark R.

// APPLICANT: Alderson, Mark R.

// APPLICANT: Smith, Craig A.

// TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor

// TITLE OF INVENTION: That Binds Thereto

// TITLE OF INVENTION: That Binds Thereto

// FILE REFERENCE: 2801-B

// CURRENT APPLICATION NUMBER: US/09/150,864A

// CURRENT FILING DATE: 1998-09-10

// PRIOR APPLICATION NUMBER: 08/060,843

// RIOR FILING DATE: 1993-05-07

// NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Alderson, Mark R.

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

TILLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION.

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2801-B

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                            Sequence 6, Application US/08236918A
Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 256 amino acids
amino acid
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Best Local Similarity 100.
Matches 11; Conservative
105 CRPGQELTKQG 115
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                                                                                                     RESULT 9
US-08-236-918A-6
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parent No. 663743.

parent No. 663743.

papelicant: Ebner, Reinhard

APPLICANT: Widen, Steven M.

APPLICANT: Widen, Steven M.

APPLICANT: Widen, Steven M.

APPLICANT: Widen, Steven M.

APPLICANT: Unition, Stephen

APPLICANT: Unition, Stephen

APPLICANT: Unition, Stephen

APPLICANT: Unition, Stephen

APPLICANT: Unition, Stephen

TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use

TITLE APPLICANT: 1999-65000

CURRENT FILING DATE: 1999-1202

EARLIER APPLICATION NUMBER: 60/12,657

EARLIER FILING DATE: 1999-07-06

EARLIER FILING DATE: 1999-07-06

EARLIER FILING DATE: 1999-07-06

EARLIER FILING DATE: 1999-07-06

EARLIER PRILICATION NUMBER: 60/124,041

EARLIER PRILING DATE: 1999-02-00

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/124,041

EARLIER APPLICATION NUMBER: 60/037,287

EARLIER PILING DATE: 1999-02-20

EARLIER PILING DATE: 1999-02-20

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER APPLICATION NUMBER: 60/003,886

EARLIER PILING DATE: 1999-03-21

EARLIER PILING DATE: 1999-03-21

EARLIER PILING DATE: 1996-03-21

EARLIER PILING DATE: 1997-03-21

EARLIER PILING DATE: 1997-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
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Pred. No. 0.00069;
0; Mismatches 1
; TITLE OF INVENTION: MURINE 4-1BB GENE; FILE REFERENCE: 740.009US1; CURRENT APPLICATION NUMBER: US/08/012,269A; CURRENT FILING DATE: 1993-02-01; PRIOR APPLICATION NUMBER: US 07/922,996; PRIOR FILING DATE: 1992-07-30; PRIOR FILING DATE: 1988-11-07; PRIOR FILING DATE: 1988-11-07; NUMBER OF SEQ ID NOS: 13; SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 7; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: An artificial peptide
US-08-012-269A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/09523323
Patent No. 6635743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.9%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-323-55
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                                                                                                                                                                                                                                PCT-US96-03965-2

Sequence 2, Application PC/TUS9603965

GENERAL INFORMATION:

APPLICANT: Kwon, Byoung Se

APPLICANT: Kang, Chang-Yuil

TITLE OF INVENTION: Monoclonal antibody against human

TITLE OF INVENTION: receptor 4-1BB

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Barnard, Brown & Michaels

STREET: 306 East State Street, Suite 220

CITY: Ithaca

STATE: NY

COUNTRY: USA

ZIP: 14850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

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COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: XWO5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08012269A; Patent No. 6362325; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                105 CRPGÓBLTKOG 115
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                                                    CRPGQELTKQG 11
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US-08-012-269A-7
                                                                                                                                                                                                           RESULT 13
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S-08-816-605-9
Sequence 9, Application US/08816605
Patent No. 5874240
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 1; Length 255;
Pred. No. 0.97;
2; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
                                     ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FLING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 9410 Key West Avenue CITY: Rockville STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
TATORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Patent No. 5874240

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Gentz, Reiner

TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 219;
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Patent No. 5674704

GENERAL INFORMATION:

APPLICANT: Alderson, Mark R.

APPLICANT: Goodwin, Raymond G.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

STREET: 51 University Street

CITY: Seattle
                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,605
FILING DATE: 13-MAR-1997
 Score 47; DB 4
Pred. No. 0.49;
                                            2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8512
Query Match 75.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 219 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                      1 CRPGOBLTKOG 11
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Gaps

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US-09-150-864A-8

US-09-150-864A-8

Sequence 8, Application US/09150864A

Sequence 8, Application US/09150864A

GENERAL INFORMATION:

APPLICANT: Alderson, Mark R.

APPLICANT: Smith, Craig A.

TITLE OF INVENTION: That Binds Thereto

TITLE OF INVENTION: That Binds Thereto

TITLE OF INVENTION: US/09/150,864A

CURRENT APPLICATION NUMBER: US/09/150,864A

CURRENT FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 08/060,843

PRIOR FILING DATE: 1993-05-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 06
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; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; CURRENT APPLICATION NUMBER: US/09/007, 097A
; CURRENT PILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-007-097-2
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Dest Local Similarity 72.7%; Pred. No. 0.97;

Matches 8; Conservative 2; Mismatches 1; Indels
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APPLICANT: Ni, Jian
APPLICANT: Reiner
APPLICANT: Ruben, Steven
TILE OF INVENTION: Tumor Necrosis Factor Receptor 5
TILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 255
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; ORGANISM: Homo sapiens (clone: hu4-1BB)
US-09-150-864A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 11, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
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Matches 8; Conservative
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                                                                                                                                                                                                                Score 47; DB 2; Length 255; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: REINER
; APPLICANT: RUBEN, SEINER
; APPLICANT: RUBEN, TUMOR NECROSIS FACTOR RECEPTOR 5
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR SECURDER CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/OCKET NUMBER: 36,373
REFERENCE/OCKET NUMBER: 36,373
REJEPHONE: (301) 309-8512
ITELEPHONE: (301) 309-8512
INFORMATION FOR.SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-09-007-097-2
; Sequence 2, Application US/09007097A
                              ;
TYPE: amino acids;
;
STRANDEDNESS: single;
;
TOPOLOGY: linear;
;
MOLECULE TYPE: protein
US-08-816-605-9
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
             INFORMATION FOR SEQ ID NO:
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US-09-578-764A-2
; Sequence 2, Application US/09578764A
; Patent No. 6569997
; GENERAL INFORMATION:
; APPLICANT: KWON, BYOUNG
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/578,764A
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; LENGTH: 255
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Sequence 2, Application US/09623545A;
Batent No. 6627200;
GENERAL INFORMATION:
TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE T
TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES
FILE REFERENCE: 30424.1USWO
CURRENT APPLICATION NUMBER: US/09/623,545A;
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: EPO 98103859.9
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 255
                                                                                      Score 47; DB 4; Length 255;
Pred. No. 0.97;
2; Mismatches 1; Indels
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                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.8%;
72.7%;
                                                                                    Query Match 75.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                               106 ČKQĞQELTKKG 116
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-578-764A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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FCT-USSC ...
Sequence 8, Applicace...
Sequence 8, Applicace...
Sequence 8, Applicace...
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
APPLICANT: Kwon, Byoung Se
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: Monoclonal antibody against human
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TITLE OF INVENTION: Monoclonal antibody against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.8%; Score 47; DB 5; 72.7%; Pred. No. 0.97; iive 2; Mismatches 1
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FILING DATE: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122, 796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922, 996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922, 996
FILING DATE: 30-JUL-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REFERENCE/DOCKET NUMBER: XWOS
TELEFHONE: 607-273-1711
TELEFAX: 607-273-2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09746359A
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Patent No. 6610286;
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Ku, Wenfeng
APPLICANT: Kelly, James D.
APPLICANT: Relly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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RESULT 25

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Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 4; Length 201;
Pred. No. 8.8;
1; Mismatches 2; Indels
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US-09-746-359A-15
Sequence 15, Application US/09746359A
Patent No. 6610286
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Kally, James D.
APPLICANT: Kally, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Julia E.
APPLICANT: Candrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Vasmin A.
APPLICANT: Chandrasekher, Vasmin A.
APPLICANT: Chandrasekher, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: GO/171,969
PRIOR APPLICATION NUMBER: GO/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2001-05-21
SPRIOR APPLICATION NUMBER: GO/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH 203
                              APPLICANT: Thompson, Penny
APPLICANT: Thompson,
APPLICANT: Thompson,
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Gagan, Maribeth A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Oc. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: 60/217,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%;
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Best Local Similarity 70.0
Matches 7; Conservative
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111.RPGMEITKDG 120
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CORGANISM: Homo sapiens
US-09-746-359A-15
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, ORGANISM: Homo sapiens
US-09-746-359A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
US-09-746-359A-67
iSequence 67, Application US/09746359A
iPatent No. 6610286
iPatent No. 6610286
iPatent No. 6610286
iPatent No. 6610286
iPatent No. 6610286
iPatent No. 6610286
iPatent Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Natural Nat
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 70
LENGTH: 135
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US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. 6610286
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52 RPGMEITKDG 61
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CORGANISM: Homo sapiens
US-09-746-359A-70
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Pan, Minhong
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P1739R1
CURRENT APPLICATION NUMBER: US/09/548,130
CURRENT FILING DATE: 2000-04-12
BARLIER FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
LENGTH: 297
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Pred. No. 14;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thompson, Penny
APPLICANT: Thompson, Penny
APPLICANT: Thompson, Penny
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Bagan, Maribeth A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Gaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Oberges, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application US/09746359A Patent No. 6610286 GENERAL INFORMATION:
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; Sequence 6, Application US/09548130
; Patent No. 6534061
                                                                                                                     Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 1
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Best Local Similarity 70.0
Est Local 7; Conservative
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; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-14
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; ORGANISM: Homo sapiens
US-09-746-359A-57
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US-09-746-359A-57
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Pred. No. 14;
1; Mismatches 2; Indels
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APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
FITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/746,359A CURRENT FILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: 60/171,969 PRIOR FILING DATE: 1999-12-23 PRIOR APPLICATION NUMBER: 60/213,341 PRIOR FILING DATE: 2000-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 307
TYPE: PRT
                                                                                                                                                              Sequence 58, Application US/09746359A Patent No. 6610286
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Kelly, James D.
Sprecher, Cindy A.
Blumberg, Hal
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Sprecher, Cindy A.
Blumberg, Hal
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                                                                                                                                                                                                                               APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eagan, Maribeth A
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PPLICANT: Foster, Donald C.
PPLICANT: Xu, Wenfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                111 RPGMEITKDG 120
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     2 RPGQELTKQG 11
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US-09-746-359A-58
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Gaps

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Sequence 7, Application US/09512363
Sequence 7, Application US/09512363
Patent No. 6503184
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
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Gaps
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; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
    APPLICANT: Randall, Troy D.
    APPLICANT: Zlotnik, Albert
    TILE OF INVENTION: MANWALIAN CELL SURFACE ANTIGENS; RELATED
    TILE OF INVENTION: REAGENTS
    NUMBER OF SEQUENCES: 8
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DNAX Research Institute
    STREET: 901 California Avenue
    CITY: Palo Alto
    STATE: California
    COUNTRY: USA
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Indels
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CIP: 94304-1104

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,423

FILING DATE: 14-AUG-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 60/023,419

FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/027,901

FILING DATE: 0.-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0612K

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 650-496-1200

THEOPMATICN FOR SEO. 1D NO: 2:
 1;
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 Mismatches
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Pred. No. 2
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Best Local Similarity 54.5
Matches 6; Conservative
     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-911-423-2
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                                                     1 CRPGQELTK 9
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         Matches
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; Sequence 3, Application US/09548130
; Patent No. 6534061
; Patent No. 6534061
; Patent No. 6534061
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P1739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.5%; Score 40; DB 4; Length 299; 77.8%; Pred. No. 20;
                                                                                                        64.5%; Score 40; DB 4; Length 297; 77.8%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/10119466
; Sequence 12, Application US/10119466
; Patent No. 6607899
; GENERAL INFORMATION:
; APPLICANT: Chui, Clarissa
; APPLICANT: Chui, Clarissa
; APPLICANT: Milton, Sean
; APPLICANT: Yan, Minhong
; APPLICANT: Yi, Sothy
; TITLE OF INVENTION: CLONING METHOD
; FILE REFERENCE: P1797
; CURRENT APPLICATION NUMBER: US/10/119,466
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/480,782
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 12
; LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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; LOCATION: 1-299
; OTHER INFORMATION:
US-10-119-466-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                          1 CRPGQELTK 9
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ORGANISM: Human
                 ; TYPE: PRT
; ORGANISM: Human
US-09-548-130-6
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us-10-067-122b-2_copy_105_115.rai

Page 12

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; TYPE: PRT
; ORGANISM: human
US-09-286-529-3
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US-09-176-200-7
; Sequence 7, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
; APPLICANT: Nu. Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT FILING DATE: 1998-10-21
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.9%; Score 39; DB 4; Length 228; Best Local Similarity 54.5%; Pred. No. 23; Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09286529
Sequence 4, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
FILE REFERENCE: PF396

CURRENT APPLICATION NUMBER: US/09/512,363

CURRENT FILING DATE: 2000-02-23

EARLIER APPLICATION NUMBER: 60/063,212

EARLIER APPLICATION NUMBER: 09/176,200

EARLIER APPLICATION NUMBER: 60/121,648

EARLIER FILING DATE: 1998-10-21

EARLIER FILING DATE: 1999-02-24

EARLIER FILING DATE: 1999-02-13

EARLIER FILING DATE: 1999-05-13

EARLIER APPLICATION NUMBER: 60/144,076

EARLIER APPLICATION NUMBER: 60/144,076

EARLIER FILING DATE: 1999-07-16

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 7

LENGTH: 228
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82 CQPGQRVESQG 92
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
US-09-176-200-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-512-363-7
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 210
                                                                                                                           Score 37; DB 3; Length 151;
Pred. No. 33;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.7%; Score 37; DB 3; Length 210; 60.0%; Pred. No. 47; 2; Indels tive 2; Mismatches 2; Indels
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Job time : 1.58219 secs
                                                                                                                         Query Match 59.7%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                         1 CRPGQELTKQ 10
                                                                                                                                                                                                                                              53 CGPGMELSKE 62
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52 CGPGMELSKE 61
; SEQ ID NO 4
; LENGTH: 151
; TYPE: PRT
; ORGANISM: human
US-09-286-529-4
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May 5, 2004, 14:40:42; Search time 4.06849 Seconds (without alignments) 749.438 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/BCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1138120 seqs, 277189581 residues
                                                                                                                                                                                                                                                                                                                                  US-10-067-122B-2_COPY_105_115
62
1 CRPGQELTKQG 11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 13, Appl	Sequence 136, App	Sequence 10, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 55, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 11, Appl	Sequence 13, Appl	Sequence 2, Appli	Seguence 9, Appli	Sequence 2, Appli	Sequence 2, Appli	
QI	US-10-067-122-13	US-09-405-032-136	US-10-027-199-10	US-10-067-122-2	US-10-067-122-7	US-10-375-680-55	US-09-739-394-2	US-10-097-330-2	US-09-739-394-9	US-09-826-212-11	US-09-935-727-13	US-09-877-336-2	US-10-097-330-9	US-10-027-199-2	US-10-170-997-2	
	14	11	13	4	1 .	15	σ	13	თ	σ	σ	10	13	13	14	
% Query Match Length DB	111	191	256	256	12	132	219	219	255	255	255	255	255	255	255	
% Query Match	100.0	100.0	100.0	100.0	91.9	75.8	75.8	75.8	75.8	75.8	75.8	75.8	75.8	75.8	75.8	
Score	62	62	62	62	57	47	47	47	47	47	47	47	47	47	47	
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ALIGNMENTS

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RESULT 1

Sequence 13, Application US/10067122

Sequence 13, Application US/10067122

Sequence 13, Application US/10067122

Sequence 13, Application US/0005121

Sequence 13, Application US/0007454

SEQUENCEAL INFORMATION:

TITLE OF INTENTION: WINTER 4-1BB GENE

TITLE OF INTENTION: WINTER: US/10/67,122

CURRENT FILING DATE: 1993-02-01

PRIOR APPLICATION UNMER: 08/012,269

PRIOR APPLICATION UNMER: 08/012,269

PRIOR APPLICATION UNMER: US/07/922,996

PRIOR APPLICATION UNMER: US/07/922,996

PRIOR APPLICATION UNMER: US/07/267,572

PRIOR APPLICATION UNMER: US/07/267,572

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PRIOR APPLICATION UNMER: US/07/267,572

PRIOR APPLICATION UNMER: US/07/267,572

WISSEL PRIOR TILING US/09/05032

SEQUENCY MATCH

Best Local Similarity 100.0%; Pred. No. 0.00027;

Matches 11; COMPENTATION:

ON CRADITICATION US/09/05032

SEQUENCE 136, Application US/09/05032

SEGUENCE 136, Application US/09/05032

SEGUENCE 136, Application US/09/05032

SEGUENCE 136, Application US/09/05032
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Query Match 100.0%; Score 62; DB 14; Length 256; Best Local Similarity 100.0%; Pred. No. 0.0075; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                               Sequence 2, Application US/10067122;
Publication No. US20030100745A1;
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung S.
TITLE OF INVENTION: MURINE 4-1BB GENE
TITLE TEFFERENCE: 740.009US1
CURRENT APPLICATION NUMBER: US/10/067,122
CURRENT FILING DATE: 2002-04
PRIOR APPLICATION NUMBER: US/02.269
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: US 07/922,996
PRIOR APPLICATION NUMBER: US 07/267,572
PRIOR APPLICATION NUMBER: US 07/267,572
PRIOR FILING DATE: 1988-11-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CRPGQELTKQG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Mus musculus US-10-067-122-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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; Publication No. US20020168719A1
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 740.013US2
; CURRENT APPLICATION NUMBER: US/10/027,199
; CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572
; CURRENT FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-06-05
; RIOR FILING DATE: EARLIER FILING DATE: 1993-09-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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APPLICANT: Amgen Inc.

TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-Dos/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/405,032
FILING DATE: 24-Sep-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378-CIP2
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 136: US-09-405-032-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Gaps

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Sequence 7, Application US/10067122

Publication No. US20030100745A1

GENERAL INFORMATION:
APPLICANT: Kwon, Byoung S.
TITLE OF INVENTION: WURINE 4-1BB GENE
FILE REFERENCE: 740.009US1
CURRENT APPLICATION NUMBER: US/10/067,122
CURRENT FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 08/012,269

PRIOR FILING DATE: 1993-02-01

PRIOR FILING DATE: 1992-07-30

PRIOR FILING DATE: 1998-11-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: An artificial peptide US-10-067-122-7
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US-10-375-680-55
; Sequence 55, Application US/10375680
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105 CRPGQELTKQG 115

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Gaps
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US-10-097-330-2

Sequence 2, Application US/10097330

Publication No. US20020127651A1

GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT

FILE REFERENCE: PF254D1C2

CURRENT APPLICATION NUMBER: US/10/097,330

CURRENT FILING DATE: 2002-03-15

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1997-03-13

PRIOR FILING DATE: 1997-03-13

PRIOR FILING DATE: 1997-03-13

PRIOR FILING DATE: 1997-03-13

PRIOR FILING DATE: 1996-03-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 2

LENGTH: 219

LENGTH: 219

LENGTH: 219

LENGTH: 219
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                                Length 219;
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                                                                            1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                  Score 47; DB 9;
Pred. No. 2.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 1
Pred. No. 2.9;
2; Mismatches
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APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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Best Local Similarity 72.7%;
Matches 8; Conservative
                                      Ouery Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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70 CKQGQELTKKG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-10-097-330-2
US-09-739-394-2
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Publication No. US20040009147A1

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Ruben, Steven M
APPLICANT: Ruben, Steven M
APPLICANT: Ullrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000E
CURRENT APPLICATION NUMBER: US/10/375,680
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,234
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09739394

Sequence 2, Application US/09739394

GENERAL INFORMATION:

GENERAL INFORMATION:

Yu, Guo-Liang

Gentz, Reiner

TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,394
FILING DATE: 19-Dec-2000
CLASSIFICATION CURNOWN>
PRIOR APPLICATION NUMBER: 09/253,549
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REFERENCE/DOCKET NUMBER: 96,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-375-680-55
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US-09-739-394-2
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RESULT 13
US-10-097-330-9
; Sequence 9, Application US/10097330
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Best Local Similarity 72.7%;
Matches 8; Conservative ;
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Best Local Similarity 72.7
Matches 8; Conservative
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US-09-935-727-13
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US-09-877-336-2
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Sequence 13, Application US/09935727

Batent No. US20020150583A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REFERENCE: PF454P2

CURRENT APPLICATION NUMBER: US/09/935,727

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-07-06

PRIOR FILING DATE: 2001-17-06

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21
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Sequence 11, Application US/09826212

Patent No. US20010021516A1

GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei

APPLICANT: Ruben, Steven

APPLICANT: Ruben, Steven

APPLICANT: Ni, Jian

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280006

CURRENT APPLICATION NUMBER: US/09/826,212

CURRENT APPLICATION NUMBER: 26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.0

SEQ ID NO 11

LENGTH: 255
           FILING DATE: «UNKNOWN»

ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF254
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8512
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
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APPLICATION NUMBER: 09/253,549
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-394-9
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Best Local Similarity 72.7%;
Matches 8; Conservative
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US-09-826-212-11
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 740.01103
CURRENT APPLICATION NUMBER: US/09/877,336
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 1998-01-14
PRIOR FILING DATE: 1998-01-14
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1995-03-23
PRIOR FILING DATE: 1995-03-23
PRIOR FILING DATE: 1993-09-16
NUMBER OF SEQ ID NOS: 10
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PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-14
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1997-01-14
SOFTWARE: PATENTIN NUMBER: 60/035,496
PRIOR FILING DATE: 1998-01-13
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
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COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/170,997
FILING DATE: 12-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/955,573
FILING DATE: 22-OCT-1997
APPLICATION NUMBER: US 08/122,796
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/122,796
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: US 08/122,996
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 08/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: ALTORNEY/AGENT INFORMATION:
                                                                                           STREET: 306 East State
CITY: Ithaca
                                                                                                                                                                                          ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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SOFTWARE: Patentin Ver. 3
                                                                                                                                            STATE: NY
COUNTRY: USA
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Publication No. US20020168719A1

GENERAL INFORMATION:
APPLICANT: Kwon, Byoung

TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS

FILE REFERENCE: 740.013US2

CURRENT APPLICATION NUMBER: US/10/027,199

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22

PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05

PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH OF THE SALVER FILING DATE: 1993-09-03
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APPLICANT: Kwon, Byoung Se
TITLE OF INVENTION: New Receptor and Related Products and
                                    APPLICANT: Ni et al.

APPLICANT: Ni et al.

TITLE ON INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
FILE REFERENCE: PF254D1C2
CURRENT APPLICATION NUMBER: US/10/097,330
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/739,394
PRIOR FILING DATE: 1999-02-22
PRIOR PPLICATION NUMBER: US 09/253,549
PRIOR PILING DATE: 1999-02-22
PRIOR PPLICATION NUMBER: US 08/816,605
PRIOR PILING DATE: 1997-03-13
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 255;
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Pred. No.
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Publication No. US20030082157A1
Publication No. US20020127651A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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ORGANISM: Homo sapiens
US-10-027-199-2
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conserv
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Publication No. US20030118546A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB Pred. No. 3.4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/10/186,643
CURRENT FILING DATE: 2002-07-02
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: KW04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/573,986 PRIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein sequence Description: Sequence Description: Seq ID NO: US-10-170-997-2
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Gaps

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) Remaining Prior Application data removed - See File Wrapper or PALM.
) NUMBER OF SEQ ID NOS: 51
) SEQ ID NO 13
) LENGTH: 255
) TYPE: PRT
) ORGANISM: Homo sapiens
US-10-418-242-13
                                                                                                                                                                          Score 47; DB 15; Length 255;
Pred. No. 3.4;
                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                           Ouery Match 75.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                         106 CKOGOELTKKG 116
                                                                                                                                                                                                                                                              1 CRPGQELTKQG 11
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APPLICANT: Gentz et al.

TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REFERENCE: PF45493

CURRENT APPLICATION NUMBER: US/10/418,242

CURRENT FILING DATE: 2003-04-18

PRIOR APPLICATION NUMBER: 09/935,727

PRIOR APPLICATION NUMBER: 09/935,727

PRIOR APPLICATION NUMBER: 60/303,224

PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-07-06

PRIOR PILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-08-02
                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                              Sequence 160, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 160
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Pred. No. 3.4;
2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,279
PRIOR FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10418242 Publication No. US20040013664A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.8%;
                                                                                                                               Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                       106 CKQGQELTKKG 116
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                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-186-643-11
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US-10-207-655-160
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Best Local Similarity
Matches 8; Conserv
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US-10-207-655-160
SEQ ID NO 11
LENGTH: 255
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APPLICANT: GERLAGA, VALEAR B.
APPLICANT: GERLAGA, VALEAR B.
APPLICANT: MILEGARA, VALEAR B.
APPLICANT: MILEGARA, VALEAR B.
APPLICANT: MILEGARA, VALEAR B.
APPLICANT: MILEGARA, GERNADA
TITLE OF INVENTION: MILEGARA B.
TITLE OF INVENTION: MILEGARA B.
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TITLE OF INVENTION: MILEGARA B.
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/199, 645
PRIOR APPLICATION NUMBER: 60/200, 025
PRIOR APPLICATION NUMBER: 60/200, 025
PRIOR APPLICATION NUMBER: 60/200, 024
PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-04-26
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PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
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PRIOR P
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184 CRPGFELTK 192
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US-10-239-663-35
; ORGANISM: Homo sapiens
US-10-104-047-2834
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; Sequence 2834, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SEQ ID NO 2834
; LENGTH: 880
; TYPE: PRT
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US-09-839-446-12
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US-10-104-047-2834
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; Sequence 6, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMPER, James N.
; APPLICANT: TOPPER, James N.
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; TITLE OF INVENTION NUMBER: 60/369876
; CURRENT FILING DATE: 2002-04-03
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.4%; Score 43; DB 14; Length 897; Best Local Similarity 88.9%; Pred. No. 66; Matches 8; Conservative 0; Mismatches 1; Indels
Query Match 69.4%; Score 43; DB 15; Length 880; Best Local Similarity 88.9%; Pred. No. 65; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Mitavi, Safia, K.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/10/239,663
CURRENT APPLICATION NUMBER: PCT/US01/09226
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR APPLICATION NUMBER: 60/192,166
PRIOR APPLICATION NUMBER: 60/192,166
PRIOR STILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,166
PRIOR SEQ ID NOWBER: 60/200,166
PRIOR SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
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Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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US-00-2989-70-14

US-00-20-298-70-14

Sequence 14, Application US/09898570

Sequence 14, Application US/09898570

SERIOR US/00-2012-66-12A1

SEPECANT: ELLERMAN, KAREN

APPLICANT: ELLERMAN, KAREN

TITLE OF INVENTION: NOVEL HUMAN RRCTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVEL HUMAN RRCTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVEL HUMAN RRCTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVEL HUMAN RRCTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVEL HUMAN RRCTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVER: 00/10-03

FILE REPERENCE: 1596-776-70-03

FRICK REILING DATE: 2000-04-64

FRICK APPLICATION NUMBER: 60/10-03

FRICK APPLICATION NUMBER: 60/20-025

FRICK FILING DATE: 2000-04-65

FRICK APPLICATION NUMBER: 60/20-025

FRICK APPLICATION NUMBER: 60/20-025

FRICK APPLICATION NUMBER: 60/20-025

FRICK APPLICATION NUMBER: 60/20-025

FRICK REILING DATE: 2000-04-19

FRICK REILING DATE: 2000-04-19

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

FRICK REILING DATE: 2000-07-03

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FRICK REILING DATE: 2001-04-19

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                                                                                                                                                                                                                                                                                               1; Indels
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OTHER INFORMATION: Description of Unknown Organism: POLYX

OTHER INFORMATION: 297832_B_1
US-09-898-570-14
                                                                                                                                                                                                                                                                                          0; Mismatches
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                         ; TYPE: PRT
; OKGANISM: Homo sapiens
US-10-406-073-6
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                          SEQ ID NO 6
LENGTH: 914
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184 CRPGFELTK 192

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| Sequence 14, Application US/0933446
| Publication No. US200006203241
| GREEKL INFORMATION: UNLESS ON THE NATIONAL DESCRIPTIONS OF THE NATIONAL DESCRIPTIONS OF THE NATIONAL DESCRIPTIONS OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATIONAL DESCRIPTION OF THE NATI
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APPLICANT: Stone, David
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APPLICANT: Stone, David
APPLICANT: MacDougall, John
FILE REFERENCE: 21402-091
CURRENT APPLICATION NUMBER: US/09/930,512
CURRENT FILING DATE: 2001-08-15
FRIOR APPLICATION NUMBER: 60/225,692
PRIOR PILING DATE: 2000-08-16
PRIOR PILING DATE: 2000-08-16
PRIOR PLILING DATE: 2000-08-18
PRIOR PLILING DATE: 2000-08-18
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                      CURRENT APPLICATION NUMBER: US/10/406,073
CURRENT FILING DATE: 2003-04-03
FRIOR APPLICATION NUMBER: 60/369876
FRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 993
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Publication No. US20040010118A1
GENERAL INFORMATION:
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APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Spaderna, Steven
APPLICANT: Gangolli, Esha A
APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Wishra, Vishnu
APPLICANT: Wernet, Corine
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Grosse, William M
Alsobrook II, John P
Liu, Xiaohong
Gerlach, Valerie L
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Smithson, Glennda
Peyman, John
Stone, David
FILE REFERENCE: MPI02-048P1RNM
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                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-15
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; Sequence 8, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMPES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: TOPPER, James N.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2002-04-05
; RIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FastESQ for Windows, Version 4.0
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US-10-406-073-15
; Sequence 15, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: VANG, Ruey-Bing
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMPER, James N.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.4%; Score 43; DB 14; Length 993; Best Local Similarity 88.9%; Pred. No. 73; Matches 8; Conservative 0; Mismatches 1; Indels
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                    PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 993
PRIOR FILING DATE: 2000-03-24
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Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-239-663-36
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                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                        Query Match 69.4%; Score 43; DB 11; Length 1006; Best Local Similarity 88.9%; Pred. No. 74; Matches 8; Conservative 0; Mismatches 1; Indels (
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US-09-898-570-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 CRPGFELTK 227
                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens US-09-930-512-18
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SEQ ID NO 16
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US-09-898-570-16
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184 CRPGFELTK 192

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CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 70
LENGTH: 135
  FILE REFERENCE: 99-108D1
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; CRGANISM: Homo sapiens US-10-424-658-70
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                                                                                                                                           FEATURE:
CIHER INFORMATION: Description of Artificial Sequence: peptide;
CIHER INFORMATION: obtained by screening randomly synthesized;
CIHER INFORMATION: peptides
US-10-220-033-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.1%; Score 41; DB 9; Length 135; 70.0%; Pred. No. 20; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                        Query Match 66.1%; Score 41; DB 14; Length 15; Best Local Similarity 80.0%; Pred. No. 2; Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, Penny
APPLICANT: Thompson, Penny
APPLICANT: Toster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Bagan, Maribeth A.
APPLICANT: Gagan, Maribeth A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: ON US20020042366Alak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEGO ID NOS: 72
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; Sequence 70, Application US/10424658
; Publication No. US20040005320A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Ku, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekher, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/09746359A Patent No. US20020042366A1
                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
LENGTH: 15
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Best Local Similarity 70.0
Matches 7; Conservative
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52 RPGMEITKDG 61
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CORGANISM: Homo sapiens
US-09-746-359A-70
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US-10-424-658-70
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Query Match 66.1%; Score 41; DB 15; Length 135; Best Local Similarity 70.0%; Pred. No. 20; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 41; DB 9; Length 196; 70.0%; Pred. No. 30; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                              APPLICANT: Thompson, Penny
APPLICANT: Thompson, Penny
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Su, Wenfeng
APPLICANT: Strecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Gaspers, Stephen R.
APPLICANT: Gaspers, Stephen R.
APPLICANT: On US20020042366Alak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 196
THENDER OF THE SET SEQ FOR WINDOWS TO SEQ ID NO 67
LENGTH: 196
                                                                                                                                                                                                                                                               Sequence 67, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
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Best Local Similarity 70.09
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                       RESULT 35
US-09-746-359A-67
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Query Match
Best Local Similarity 70.u-
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Best Local Similarity 70.0
Matches 7; Conservative
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US-09-912-672A-16
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         US-09-912-672A-16
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US-10-424-658-59
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
      APPLICANT: FOSLET, DOMAIN C.
APPLICANT: Xu, Wenfeng
APPLICANT: Slumberg, Hal
APPLICANT: Chandrasekher, Yasmin A.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108D1
CURRENT APPLICATION NUMBER: US/10/424,658
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASLEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. US20020042366Alak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/746,359A;
CURRENT FILING DATE: 2001-05-21;
PRIOR APPLICATION NUMBER: 60/171,969;
PRIOR FILING DATE: 1999-12-23;
PRIOR APPLICATION NUMBER: 60/213,341;
PRIOR FILING DATE: 2000-06-22;
NUMBER OF SEQ ID NOS: 72;
COFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/09746359A Patent No. US20020042366Al GENERAL INFORMATION:
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70.0%; Pred
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APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
Donald C.
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Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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106 RPGMEITKDG 115
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111 RPGMEITKDG 120
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US-09-746-359A-59
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LENGTH: 201
TYPE: PRT
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Gaps
Sequence 16, Application US/09912672A;
Sequence 16, Application US/09912672A;
Batent No. US20020164689A1;
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
CURRENT APPLICATION NUMBER: US/09/912,672A;
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/475,541
PRIOR APPLICATION NUMBER: 09/475,541
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%; Score 41; DB 9; Length 201; 70.0%; Pred. No. 31; 2; Indels tive 1; Mismatches 2; Indels
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US-09-925-055D-35

Sequence 35, Application US/09925055D

Publication No. US20030157096A1

GENERAL INFORMATION:

APPLICANT: Kindevogel, Wayne R.

APPLICANT: Topouzis, Stavros

TITLE OF INVENTION: SOLUBLE ZCYTORII CYTOKINE RECEPTORS

FILE REFERENCE: 00-56

CURRENT FILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-08-08

PRIOR FILING DATE: 2000-12-01

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 35

LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Blumberg, Hal
APPLICANT: Chandrasekher, Yasmin A.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Publication No. US20040005320A1
GENERAL INFORMATION:
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RESULT 38

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 5, 2004, 14:34:41; Search time 1.31849 Seconds (without alignments) 802.512 Million cell updates/sec Run on:

US-10-067-122B-2_COPY_105_115 62 1 CRPGQELTKQG 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	igen	lymphocyte activat	he1	e:1	tical	period clock prote	goo	protamine - fruit	protamine - fruit	ntigen	ผ	potassium channel	hypothetical prote	fibrillin-1 precur	30S ribosomal prot	nucleoprotein - he	nucleoprotein - he	nucleocapsid prote	embryo kinase 5 -	hypothetical prote	plexin 1 precursor	ED:	male germ-line spe	protamine - fruit	port	- ute		enoyı-c	hypothetical prote
SOMMAKIES	. Д.	3239	I38426	3065	VHVNIH	T34561	UMMS	E86451	S52156	S52158	I49054	S54592	T17367	T25933	A55624	AB2148	VHVNHS	JQ1531	S34562	A56599	T27283	JC4980	B53435	852155	852157	AE0740	S06075	T49856	C70873	AH2016
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NADH2 dehydrogenas	dehydrogena		-			NADH2 dehydrogenas		NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	
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348	348	348	348	348	348	348	348	348	. 4 . 8	348	348	348	348	34.8	348	
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ALIGNMENTS

 RESULT 1 B32393 T-cell antigen 4-1BB precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C:Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 21-Jul-2000
 C, Accession: B32393; I48879 — R; Kwon, B.S.; Weissman, S.M. Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989 A; Title: cDNA sequence of two inducible T-cell genes. A; Fitle: cDNA sequence of two inducible T-cell genes.
Afacession: B32393 A;Molecule type: mRNA A;Residues: 1-256 <kwo> A;Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122 B;Woor B C · Kozak C A · Kim, K.K.; Pickard, R.T.</kwo>
 J. mmunol. 152, 2256-2262, 1994 A; Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB. A; Reference number: 148879; MUID:94179805; PMID:8133039 A; Accession: 148879
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-256 <res> A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178</res>
 C;Genetics: A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1 C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: transmembrane protein C;Keywords: transmembrane protein F;1-23/Domain: signal sequence #status predicted <sig> F;24-256/Product: 4-1BB protein #status predicted <mat></mat></sig>
Query Match Best Local Similarity 100.0%; Pred. No. 0.00085; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CRPGOELTKOG 11
 RESULT 2 138426 Lymphocyte activation-induced receptor ILA precursor - human C;Species: Homo sapiens (man) C;Date: 29-May-1998 #text_change 01-Dec-2000 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C;Accession: 138426; JT0752 R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; Rc Eur. J. Immunol. 24, 2219-2227, 1994 A;Title: Molecular and biological characterization of human 4-1BB and its ligand. A;Reference number: 138426; MUID:94374434; PMID:8088337 A;Accession: 138426 A;Accession: I38426 A;Accession: Lanslated from GB/EMBL/DDBJ A;Molecule type: mRNA

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Gaps

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C;Accession: A24403
R;Shin, H.S.; Bargiello, T.A.; Clark, B.T.; Jackson, F.R.; Young, M.W.
Nature 317, 445-448, 1985
A;Title: An unusual coding sequence from a Drosophila clock gene is conserved in vertebra A;Reference number: A24403; MUID:86014384; PMID:2413365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-713 <SHI>
A;Residues: 1-713 <SHI>
A;Cross-references: GB:X02966; GB:M12039; NID:g55125; PIDN:CAA26710.1; PID:g1334150
C;Comment: Mutations within the per locus of the fruit fly affect a variety of natural bi
logous locus with multiple tandem repeats of nucleic acid hexamers (ACNGGN, TCAGGC) that
C;Comment: The serine residues of the S-G repeats found in certain proteoglycans are atta
C;Superfamily: period clock protein; EGF homology
C;Keywords: circadian rhythm; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable copia-type polyprotein, 28768-32772 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Homo sapiens (man)
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T34561
R.Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A;Reference number: Z21540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           period clock protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86451
                                            Length 413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residence 17.0: many
A; Residences: EMBL:AL122079
A; Experimental source: adult testis; clone DKFZp434L1050
C; Genetics:
A; Note: DKFZp434L1050.1
                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp434L1050.1 - human (fragment)
                                          DB 1;
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB;
Pred. No. 37;
1; Mismatches
                                                                                                        Mismatches
                                          61.3%; Score 38;
87.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.3%;
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                               ||||:|||
183 RPGQKLTK 190
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Best Local Similarity
7; Conserve
                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                             2 RPGQELTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRPGQELTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T34561
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                                                                                                                                                                                                                        A; Residues: Lype: man, A; Residues: L106, W, 108-255 <SCH>
A; Residues: Il-106, W, 108-255 <SCH>
C; Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro C; Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;234,235/Binding site: carbohydrate (Thr) (covalent) (by casein kinase II) #status predicted F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
                                                    Rischwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne A;Reference number: JT0752; MUID:94085794; PMID:8262389
A;Accession: JT0752
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable RNA helicase - Molluscum contagiosum virus 1
N;Alternate names: MCO50R
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Nov-2000
C;Accession: T30652
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: Z20876; MUID:96325459; PMID:8670425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rigilmore Jr., R.D.; Leong, J.C.
Virology 167, 644-648, 1988
A;Title: The nucleocapsid gene of infectious hematopoietic necrosis virus, a fish rhabdo
A;Reference number: A31834; MUID:89073771; PMID:3201758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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A,Molecule type: DNA
A,Residues: 1-684 <SEN>
A;Cross-references: EMBL:U60315; NID:g1491943; PIDN:AAC55178.1; PID:g1491993
C;Superfamily: vaccinia virus I8 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleoprotein - infectious hematopoietic necrosis virus
N/Alternate names: nucleocapsid protein
C;Species: infectious hematopoietic necrosis virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
                        Cross-references: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C;Keywords: nucleocapsid; nucleoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; Length 684; Pred. No. 37; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%;
63.6%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 CKQGQELTKKG 116
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<RES>
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-413 <GIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A31834
R; Gilmore Jr., R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A31834
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Gaps

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A,Gene: FlyBase:Mst35Bb
A,Cross-references: FlyBase:FBgn0013301
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                                                                                               Query Match
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552156
protamine - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Dacesion: 552156
R;Russell, S.R.
submitted to the EMBL Data Library, November 1994
A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like m
A;Reference number: 552156
A;Accession: 552156
A;Accession: 552156
A;Accession: 552156
A;Accession: 552156
A;Accession: 552156
A;Accession: 552156
A;Coss-references: EMBL:Z46784; NID:g608697; PID:g608698
C;Genetics:
A;Cross-references: EMBL:Z46784; NID:g608697; PID:g608698
A;Cross-references: FlyBase:FBgn0013301
A;Cross-references: FlyBase:FBgn0013301
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, D.; Yu, G.; Eraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues: preliminary
A;Molecule types
A;Molecule types
A;Molecule types
A;Molecule types
A;Cross-references: GB:AE005172; NID:g10092575; PIDN:AAG12968:1; GSPDB:GN00141
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
C;Accession: S52158
R;Russell, S.R.
submitted to the EMBL Data Library, November 1994
A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like 1
A;Recession: S52158
A;Accession: S52158
A;Cross-references: EMBL: Z46785; NID:g608701; PID:g608702
C;Genetics:
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Pred. No. 1e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 1
C,Superfamily: retrovirus-related polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 7; Conservative
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1096 PGQKLTKAG 1104
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bystyle by the protein YMR285c - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein YM8021.11c

C.Speciaes: Saccharomyces cerevisiae

C.Date: 08-Unl-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C.Accession: 554592; A42461

R.Pearson, D., Bowman, S.

Submitted to the EMBL Data Library, May 1995

A.Reference number: 554582

A.Reference number: 554582

A.Residues: 1-515 <-PBA>

A.Reference serial AB972

A.Residues: 1-515 <-PBA>

A.Residues: 1-515 <-PBA>

A.Residues: 1-515 <-PBA>

A.Residues: 1-515 <-PBA>

A.Residues: 1-515 <-PBA>

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A.Residues: 1-515 <-PBA>

A.Residues: 1-515 <-PBA>

A.Residues: 1-68, A'A', 70-86, W', 88, ARAA', 93, YQKT', 98-105, 'Q' <-XAN>

A.Residues: 1-68, A'A', 70-86, W', 88, ARAA', 93, YQKT', 98-105, 'Q' <-XAN>

A.Residues: 5GD:NGL2

A.Residues: 5GD:NGL2

A.Residues: SGD:NGL2

A.Residues: SGD:NGL2

A.Residues: SGD:NGL2

A.Residues: SGD:NGL2

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                                                                                                                                                                                                                                                                                                                                                                                           Ly-49G.2 antigen - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Mar-2000
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Mar-2000
C; Accession: 149054
A; Title: Ly-49 multigene family expressed by IL-2-activated NK cells.
A; Reference number: 149049; MuID:9430068; PMID:8027540
A; Reference number: 149054
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-203 <RES>
A; Cross-references: EMBL:U10095; NID:g533497; PIDN:AAA50223.1; PID:g533498
C; Superfamily: natural killer cell receptor P1; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C; Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c
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59.7%; Score 37; DB 2; Length 110; 54.5%; Pred, No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%; Score 37; DB 2; Length 203; 66.7%; Pred. No. 30; 2; Indels tive
                                                                         3; Indels
                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                 Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                             69 CAPSQKCSKQG 79
                                                                                                                                               1 CRPGOELTKOG 11
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A;Molecule_type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C;Genetics:
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                                                                                                                                                                               A,Gene: Fbn-1
C,Superfamily: fibrillin; EGF homology
F;1201-1236/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                            Query Match 59.7%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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|31 CRPGEEI 137
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                                             A,Status: preliminary
                    A;Accession: A55624
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                                                                        PESULT 12
T17367

potassium channel protein elk1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17367
R;Shi, W; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.
J; Physiol. 511, 675-682, 1998
A;Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in
A;Reference number: Z18731; MUID:98382545; PMID:9714851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abbrillin-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 24-Nov-2003
C;Accession: A55624
C;Accession: A55624
R;Yin, W.; Smiley, B.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A;Fitle: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge
A;Reference number: A55624; MUID:95130561; PMID:7829516
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A;Molecule type: mRNA
A;Residues: 1-1102 <SHI>A;Cross-references: EMBL:AF061957; NID:g3659689; PID:g3659690; PIDN:AAC61520.1
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A;Molecule type: DNA
A;Residues: 1-1372 <MUR>
A;Residues: 1-1372 <MUR>
A;Cross-references: EMBL:UB0815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W02C12.1
A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein W02C12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25933
R;Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid W02C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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C;Function:
A;Description: may play a role in the sympathetic nervous system
C;Keywords: potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1102;
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A; Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
  477 CRGFLRMPPGNEMTKHG 493
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Best Local Similarity 54.5%;
Matches 6; Conservative ;
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Best Local Similarity 60.0
Matches 6; Conservative
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1098 CKPGQFLVKE 1107
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A;Gene: CESP:W02C12.1
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N'Alternate manes: nucleocapsid protein
C'Species: hemorrhagic septicemia virus
C'Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C'Accession: A36651
R'Bernard, J.; Lecocq-Xhonneux, F.; Rossius, M.; Thiry, M.E.; de Kinkelin, P.
A;Title: Cloning and sequencing the messenger RNA of the N gene of viral haemorrhagic sep
A;Reference number: A36651; MUID:90362052; PMID:2202782
A;Accession: A36651
A;Molecule type: mRNA
A;Residues: 1-404 <BER>
A;Cross-references: GB:D00687; NID:g222771; PIDN:BAA00591.1; PID:g222772
                                                                                                                                                                                         RiKaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A; Reference number: AB1807; MUID:21595285; PMID:11759840
30S ribosomal protein S4 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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;Molecule type: DNA
;Residues: 1-202 <KUR>
;Cross-references: GB:BA000019; PIDN:BAB74436.1; PID:g17131830; GSPDB:GN00179;
;Experimental source: strain PCC 7120
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C/Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C/Keywords: nucleocapsid; nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.1%; Score 36; DB 2; Length 202; Best Local Similarity 71.4%; Pred. No. 45; Matches 5; Conservative 2; Mismatches 0; Indels
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C/Superfamily: Escherichia coli ribosomal protein S4
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Gaps

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Page 5
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plexin 1 precursor - mouse

C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Nov-1999
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Nov-1999
C; Accession: JC4980
R; Kameyama, T: Murakami, Y:, Suto, F:; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 524-529, 1996
A; Title: Identification of a neuronal cell surface molecule, plexin, in mice.
A; Reference number: JC4980; MUID:96400291; PMID:8806667
A; Accession: JC4980
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
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A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71
A; Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor-A, Reference number: A56599; MUID:92144672; PMID:1664238
A, Accession: A56599
A, Status: preliminary
A; Molecule type: MRNA
A; Residues: 1-995 < PAS>
A; Residues: 1-995 < PAS>
A; Residues: 1-995 < PAS>
A; Residues: 1-995 < PAS>
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A; Resi
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T27283
R; Ainscough, R.
Submitted to the EMBL Data Library, September 1999
A; Reference number: Z20336
A; Accession: T27283
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1620 <WIL>
A; Residues: 1-1620 <WIL>
A; Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A; Experimental source: clone Y64G10A
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Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2;
Pred. No. 1.9e+02;
1; Mismatches 4
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Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                 RESULT 17
JO1531

mucleoprotein - hemorrhagic septicemia virus (strain Makah)

N,Alternate names: nucleocapsid protein
C;Species: hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Accession: JO1531; S11836
R;Bernard, J; Bremont, M.; Winton, J.
J. Gan. Virol. 73, 1011-1014, 1992
A;Title: Nucleocapsid gene sequence of a North American isolate of viral haemorrhagic se
A;Reference number: JO1531; MUID:92341050; PMID:1634868
A;Accession: JO1531
A;Molocasion: JO1531
A;Molocasion: JO1531
A;Residues: 1-404 <br/>A;Residues: 1-404 <br/>A;Residues: EMBL:X59241; NID:960410; PIDN:CAA41930.1; PID:g60411
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C;Keywords: nucleocapsid; nucleoprotein
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$34562
nucleocapsid protein - hemorrhagic septicemia virus
C; Species: hemorrhagic septicemia virus
C; Species: hemorrhagic septicemia virus
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C; Accession: 834562
R; Schuetze, H.
submitted to the EMBL Data Library, June 1993
A; Reference number: 834562
A; Reference number: 834562
A; Accession: 834562
A; Accession: 834562
A; Molecule type: DNA
A; Cross-references: EMBL: X73873; NID:g395126; PIDN: CAA52077.1; PID:g395127
C; Genetics:
A; Gene
C; Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C; Keywords: nucleocapsid
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A56599
embryo kinase 5 - chicken
N;Alternate names: receptor tyrosine kinase Cek5
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Dapecies: Gallus gallus (chicken)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
C;Accession: A56599
R;Pasquale, E.B.
Cell Regul. 2, 523-534, 1991
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184 RPGQKITK 191
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184 RPGQKITK 191
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184 RPGQKITK 191
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protamine - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1998
C;Accession: S52157
C;Accession: S52157
C;Accession: Data Library, November 1994
A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like mc A;Reference number: S52155
A;Accession: S52157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <RUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable exported protein STY2079 [imported] - Salmonella enterica subsp. enterica serovar C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: A50740 C; Accession: A50740 R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A; Reference number: AB0502; MUID:21534947; PMID:11677608
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S06075
uncI protein - Vibrio alginolyticus
C;Species: Vibrio alginolyticus
C;Species: Vibrio alginolyticus
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Oct-1999
C;Accession: S06075
R;Krumholz, L.R.; Esser, U.; Simoni, R.D.
Nucleic Acids Res. 17, 7993-7994, 1989
A;Title: Nucleotide sequence of the unc operon of Vibrio alginolyticus.
A;Reference number: S06075; MUID:90016889; PMID:2529481
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A;Gene: FlyBase:Mst35Ba
A;Cross-references: FlyBase:Fbgn0013300
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Pred. No. 40;
2; Mismatches
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Best Local Similarity 54.5%;
Matches 6; Conservative
                 44 CAPROKCSKQG 54
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69 CAPROKCSKOG 79
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A;Molecule type: DNA
A;Residues: 1-117 <PAR>
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A; Residues: 1-189, 558-721, 'P', 723-738, 'D', 740-829, 'L', 831-1100, 'Q', 1102-1636, 'L', 1638-16
418, 'H', 2420-2499, 'L', 2501-2550 <LE2>
A; Cross-references: EMBL: X73956
A; Cross-references: EMBL: X73956
Submitted to the EMBL Data Library, December 1992
A; Description: Tdentification of membrane associated proteins in Trypanosoma brucei enco
A; Reference number: S34394
A; Accession: S34395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Trypanosoma bruce;
Date: 26-May-1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999
Accession: B53435; S34395
Lee, M.G.S.; Russell, D.G.; D'Alesandro, P.A.; Van der Ploeg, L.H.T.
Biol. Chem. 269, 8408-8415, 1994
Ifitle: Identification of membrane-associated proteins in Trypanosoma bruce; encoding;Reference number: A53435; MUID:94179225; PMID:8132566
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C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1998
C; Accession: S52155
R; Russell, S.R.
submitted to the EMBL Data Library, November 1994
A; Description: Drosophila melanogaster mst35B genes encode very similar protamine like A; A; Reference number: S52155
A; Accession: S52155
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N;Alternate names: membrane-associated protein Tb-292
C;Species: Trypanosoma brucei
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                                                                                            Length 1894;
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Pred. No. 32;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Mosidues: 1-2550 <IEE>
A;Cross-references: EMBL:X73956; NID:g393395; PID:g393396
C;Keywords: tandem repeat
F;74-557/Region: 8-residue repeats (A-R-L-R-A-E-E-E)
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                                                                                  58.1%; Score 36; DB 2; Le 77.8%; Pred. No. 3.38+02; tive 0; Mismatches 2;
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A/Cross-references: FlyBase:FBgn0013300
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Best Local Similarity 54.5%;
Matches 6; Conservative 5
F;1266-1268/Region: hydrophilic
                                                                           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: mRNA
A;Residues: 1-85 <RUS>
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hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)

C, Species: Nostoc sp. PCC 7120

A; Note: Nostoc sp. PCC 7120

A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 24-Nov-2003

C; Accession: AH2016

R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Reference number: AB1807; MUID:21595285; PMID:11759840

A; Reference number: AB1807; MUID:21595285; PMID:11759840

A; Accession: AH2016

A; Actus: preliminary

A; Molecule type: DNA

A; Residues: 1-303 < KUR>
A; Residues: 1-303 < KUR>
A; Expes: references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179

A; Expes: mental source: strain PCC 7120

C; Genetics:
A; Gene: all1686
C; Superfamily: tartrate-resistant acid phosphatase
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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C;Species: mitochondrion Julidochromis marlieri
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Pred. No. 99;
1; Mismatches
Pred. No. 94;
L; Mismatches
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Local Similarity 70.0%;
nes 7; Conservative
77.8%;
   Best Local Similarity 77.8
Matches 7; Conservative
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Best Local S:
Matches 7
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Matches
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C;Species: Motobacterium tuberculosis
C;Date: 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: C70873
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Cantles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: Broindinary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-285 <COL>
A;Residues: 1-285 <COL>
A;Residues: 1-285 <COL>
A;Experimental source: Strain H37RV
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable Alp11 homolog of tubulin-folding cofactor B [imported] - Neurospora crassa probable Alp11 homolog of tubulin-folding cofactor B [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;Accession: T49856 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000 A;Reference number: Z5502 A;Acession: T49856 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-240 <SCH> A;Acesidues: 1-240 <SCH> A;Acesidues: 1-240 <SCH> A;Cross-references: EMBL:AL356833; GSPDB:GNC0116; NCSP:B24P11.120 A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;G
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          A;Accession: S06075
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-129 <KRU>
A;Cross-references: EMBL:X16050; NID:g48331; PIDN:CAA34174.1; PID:g48332
C;Genetics:
A;Gene: uncl
C;Superfamily: uncl protein
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Pred. No. 46;
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Pred. No. 81;
3; Mismatches
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2; Mismatches
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Matches 6; Conservative
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RPGRELARO 15
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A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-348 <KOC>
A;Cross-references: EMBL:U07260; NID:g463966; PID:g463967; PIDN:AAC59809.1
A;Experimental source: strain T32a; PSU
                                                                                                                                                         56.5%; Score 35; DB 2; Length 348; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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A;Molecule type: DNA
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                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                         267 QELTKÓG 273
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T14206
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Tanganicodus irsacae mitochondri
C;Species: mitochondrion Tanganicodus irsacae
C;Date: 20-Sep-1999 #semianca variation
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14034
R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A;Reference number: Z17790; MUID:96360498; PMID:8747298
A;Reference number: Z17790; MUID:96360498; PMID:8747298
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <KOC>
A;Cross-references: EMBL:U07249; NID:9463944; PID:9463945; PIDN:AAC59798.1
A;Berperimental source: strain Tla; PSU
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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Superfamily: NADH dehydrogenase (ubiquinone) chain 2
.Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Nile tilapia mitochondrion C; Species: mitochondrion Tilapia nilotica, Oreochromis niloticus (Nile tilapia) C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002 C; Accession: T14118

Ri Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F. Mol. Phylogenet. Evol. 4, 420-432, 1995

A; Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish. A; Reference number: Z17790; MUID:96360498; PMID:8747298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: mitochondrion Tanganicodus irsacae;
;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
;Accession: T14206
;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
ol. Phylogenet. Evol. 4, 420-432, 1995
;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.;Reference number: Z17790; MUID:96360498; PMID:8747298
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;Residues: 1-348 -KCC>
;Cross-references: EMBL:U07265; NID:g463976; PID:g463977; PIDN:AAC59814.1
;Experimental source: strain T13a; PSU
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A,Cross-references: EMBL:U07258; NID:g463962; PID:g463963; PIDN:AAC59806.1
A,Experimental source: strain T77a; isolate PSU
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.5%; Score 35; DB 2; Length 348 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 0; Mismatches 0; Indels
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Paracyprichromis brieni mitochond C; Species: mitochondrion Paracyprichromis brieni
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T14128
R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A;Reference number: Z17790; MUID:96360498; PMID:8747298
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  Length 348;
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1.1e+02;
Query Match 56.5%; Score 35; DB 2; Length 348 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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RESULT 39
T14216
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Xenotilapia flavipinnus mitochonc C, Species: mitochondrion Xenotilapia flavipinnus
C, Species: mitochondrion Xenotilapia flavipinnus
C, Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C, Accession: T14216
R, Kocher, TD.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A; Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A; Reference number: Z17790; MUID:96360498; PMID:8747298
A; Reference number: Z17790; MUID:96360498; PMID:8747298
A; Residues: 1-348 < kCC>
A; Catus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-348 < kCC>
A; Catus: preliminary and complexion of NADH dehydrogenase (ubiquinone) chain 2
C; Genetics:
A; Genetics: A; Genetics: SGC1
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C; Keywords: membrane-associated complex; mitochondrion;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-348 <KOC>
A;Cross-references: EMBL:U07266; NID:g463978; PID:g463979; PIDN:AAC59817.1
A;Experimental source: strain T49a; PSU
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Superfamily: NADH dehydrogenase (complex; mitochondrion; NAD; oxidative phosphorylation; c
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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T13839
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Buccochromis lepturus mitochondr
C; Species: mitochondrion Buccochromis lepturus
C; Species: mitochondrion Buccochromis lepturus
C; Species: mitochondrion Buccochromis lepturus
C; Accession: T13839
R; Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evolution of MADH dehydrogenase subunit 2 in East African cichlid fish.
A; Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A; Reference number: Z17790; MUID:96360498; PMID:8747298
A; Accession: T13839
A; Accession: T13839
A; Accession: T13839
A; Accession: T3839
A; Accession: T3839
A; Accession: T3848
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-348
A; Cross-references: EMBL:U07241; NID:9463928; PID:9463929; PIDN:AAC59788.1
C; Genetics:
C; Genetics:
A; Genome: mitochondrion
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Telmatochromis temporalis mitoch
C;Species: mitochondrion Telmatochromis temporalis
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14209
K;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A;Reference number: 217790; MUID:96360498; PMID:8747298
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T14122
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Ophthalmotilapia ventralis mitoc C; Species: mitochondrion Ophthalmotilapia ventralis C; Species: mitochondrion Ophthalmotilapia ventralis C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002 C; Accession: T14122
Kol. Phylogenet. Evol. 4, 420-432, 1995
Mol. Phylogenet. Evol. 4, 420-432, 1995
A; Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish. A; Reference number: Z17790; MUID:96360498; PMID:8747298
A; Accession: T14122
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1348 < KOC>
A; Residues: Day AKCS
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C,Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A,Experimental source: strain T10a; isolate PSU
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T14200
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Pseudotropheus sp. mitochondrion
C;Species: mitochondrion Pseudotropheus sp.
C;Species: mitochondrion Pseudotropheus sp.
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14200
R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.
Mol. Phylogenet. Evol. 4, 420-432, 1995
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.
A;Reference number: Z17790; MUID:96360498; PMID:8747298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T14200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <KOC>
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S Q

5 QELTKQG 11 ||||||| 267 QELTKQG 273

Search completed: May 5, 2004, 14:41:21 Job time : 1.31849 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 5, 2004, 14:30:56 ; Search time 0.866438 Seconds (without alignments) 661.065 Million cell updates/sec

US-10-067-122B-2_COPY_105_115 62 1 CRPGQELTKQG 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	i G	D20334 mus musculu	Q07011 homo sapien	stror	Q9hav5 homo sapien	mus n	10 10 10 10 10 10 10 10 10 10 10 10 10 1	infe		uns n	homo sap	oryzi		P59111 mus musculu	Q8r2v3 mus musculu			Q96142 homo sapien			апарає	viral hem	viral b	gallus	mus mus		vibrio		P48175 oncorhynchu	35924	ž	96100	49735	41184	
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shigella fl	054177		TGT_SHIFL	Н	375	54.8	34	45
salmonella	Q8zrd8		TGT_SALTY	~	375	54.8	3.4 4.	44
salmonella	Q828y0		TGT_SALTI	~	375	54.8	9.4 4.	43
escherichia	P19675		TGT_ECOLI	, ,	375	54.8	34	42
yersinia pe	Q8zc33		TGT YERPE	-	374	54.8	34	41
homo sapien	P43362		MAG9_HUMAN	~	315	54.8	34	40
homo sapien	Q9y5u5		TR18_HUMAN	-1	241	54.8	34	39
streptomyce	004942		AFQ1_STRCO	Н	225	54.8	34	38
bacillus su	P39788		END3 BACSU	~	219	54.8	34	37
schistosoma	P27591		IM23_SCHJA	٦	218	54.8	34	36
gallus gall	P07583		LEG4 CHICK	~	134	54.8	34	35
gallus gall	004205		TENS CHICK	1	1744	56.5	32	34

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encilled and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).

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family.";
Gene 134:295-298(1993).
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PIR; B32393; B32393.

PDB; 1D0J; 26-SEP-01.

MGD; MGI:1101059; Tnfrsf9.

InterPro; IPR001368; TNFR c6.

Pfam; PF00020; TNFR c6; 1.

SMART; SM00208; TNFR; 2.

PROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.

Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94374434; PubMed=8088337;
Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.; "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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0
                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 1; Length 256; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels
                                                                                                                                               SUPERFAMILY MEMBER 9. EXTRACELLULAR (POTENTIAL).
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MEDLINE=94085794; PubMed=8262389; Schwarz H., Tuckwell J., Lotz M.;

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NEDLINE-SIGNER N. A. A. Brown N. A. Browner From N. A. Browner From N. A. Brausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina R.B., Bonaldo M.F., Casavant T.L., Scheetz T.B. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
MEDLINE=21662677; PubMed=11804328;
Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
"A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-médiated signal transduction.";
Mol. Cells 12:304-312(2001).
-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
-!- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand.";
J. Exp. Med. 187:1849-1862(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98078711; Pubmed=9418902;
Arch R.H., Thompson C.B.;
"4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB.";
Mol. Cell. Biol. 18:558-565(1998).
                                                                                                                                                                                                    Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.; "Characterization of human homologue of 4-1BB and its ligand."; Immunol. Lett. 45:67-73(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH TRAFI AND TRAF2.
MEDLINE=98270914; PubMed=9607925;
Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
Watts T.H.;
                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       rearce A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRR-repeat protein 1/LRR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
                                                                                                                                                                                   WEDLINE=95347766; PubMed=7622190
                                                                                 Schwarz H.;
Submitted (MAR-1999)
                                                                                                                                           SEQUENCE FROM N.A.
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Score 42; DB 1; Length 639;
Pred. No. 3.9;
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110 306
307 419
420 531
532 573
97 198
1 201
7 207
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71893 MW; S
                                                                                                                                                                                                                                                                                                  67.7%;
 Strongylocentrotus.
NCBL_TaxID=7668;
                                                                                                                                                                                                                                                                                                       Best Local Similarity
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Query Match
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.sen.edu.
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                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        Score 47; DB 1; Length 255;
Pred. No. 0.16;
2; Mismatches 1; Indels
DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
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Best Local Similarity 72.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                            TISSUE=EMDYO;
MEDLINE=94215496; PubMed=8162855;
Hwang S.P.L., Partin J.S., Lennarz W.J.;
Hwang S.P.L., Partin J.S., Lennarz W.J.;
Hwang S.P.L., Partin J.S., Lennarz W.J.;
"Characterization of a homolog of human bone morphogenetic protein 1 in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
Development 120:559-568(1994).
-! TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in hatched blastula.
-! DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.
-! SIMILARITY: Belongs to peptidase family M12A.
-! SIMILARITY: Contains 1 EGF-like domain.
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CUB 2.

CUB 2.

CUB 2.

EGF-LIKE, CALCIUM-BINDING (POTENTIAL).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

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N-LINKED (GLCNAC. . ) (POTENTIAL).

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STRAIN-BALB/C;
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TR18_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fetal kidney;
MEDLINE=20495245; PubMed=11039935;
Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A., de Vos A.M., Gao W.-Q., Dixit V.M.;
"Two-amino acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors.";
Science 290:523-527(2000).
                                                                                                                                                                                                                                                     Q9HAV5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member XEDAR (X-linked ectodysplasin-A2 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 300276; -. GO: 0005031; F: tumor necrosis factor receptor activity; NAS.
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  Indels
  3,
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  Mismatches
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  7; Conservative
                                                                                                       559 CRPGYELSSDG 569
                                                                                                                                                                                                                              STANDARD;
                                                  1 CRPGOELTKOG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   XEDA HUMAN
                                                                                                                                                                              Matches
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MEDLINE=20256302; PubMed=10798444; S., Giunchi L., Cupelli A., Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A., Delfino D., Migliorati G., Riccardi C.; "Gene structure and chromosomal assignment of mouse GITR, a member of the tumor necrosis factor/nerve growth factor receptor family."; DNA Cell Biol. 19:205-217(2000).
                                                                                                                                                                                                                                                                      (TYPE III MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                     TNER-CYS 1.

TNER-CYS 2.

TNER-CYS 3.

BY SIMILARITY.

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W; OB71127C6C48240C CRC64;
GO; GO:0008544; P:epidermal differentiation; NAS.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR NGFR_1; 2.
PROSITE; PS50050; TNFR NGFR_2; 2.
Receptor; Developmental protein; Differentiation; Transmembrane; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9732352; PubMed=9177197;
Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A., Moraca R., Migliorati G., Riccardi C.;
"A new member of the tumor necrosis factor/nerve growth factor receptor family inhibits T cell receptor-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIS MOUSE STANDARD; PRT; 228 AA.

78574; Q9JKR1; Q9JKR2; Q9JKR3;
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor (Glucocorticoid-induced TNFR-related protein).

TNFRSF18 OR GITR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.5%; Score 40; DB 1; Length 297; 77.8%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                     (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.1;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32728 MW;
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nes 7; Conservative
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297 AA;
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                                                                                                                                                                                                                                                                           139
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ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP -> VLLQRPSHSRRCSCQLRMLAASSSLRRNAGSRQKKSVI WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW

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228
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                                                                                                                                                                                                                                                                                                                                              Molluscipoxvirus.
NCBI_TaxID=10280;
189
                                                             189
                                                                                                                        Query Match
Best Local S
Matches 6
VARSPLIC
                                                            VARSPLIC
                                                                                                     SEQUENCE
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                                                                                                                                                                                                                    RESULT 6
NTP2 MCV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCSOFGFLTWFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM
AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAED
ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
                                         cells
                                                                                                                                                                                                                                                  -!- INDUCTION: Upregulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
Brunetti L., Migliorati G., Riccardi C., "Identification of three novel mRNA splice variants of GITR."; Cell Death Differ. 7:408-410(2000).
-!- FUNCTION: Receptor for TNFSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial and in the regulation of T cell receptor-mediated cell death. Mediated NF-kappa-B activation via the TRAFZ/NIK pathway (By
                                                                                        TRAFE (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B C); secreted (isoform D).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
                                                                     similarity). SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                         Name=D;
IsoId=035714-4; Sequence=VSP_006509;
TISSUE SPECIFICITY: Preferentially expressed in activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF109216; AAF14231.1; -.
EMBL; AF229432; AAF61566.1; -.
EMBL; AF229433; AAF61567.1; -.
EMBL; AF229434; AAF61568.1; -.
EMBL; AF229434; AAF61568.1; -.
EMBL; AF229434; AAF61568.1; -.
EMBL; AF229434; AAF61568.1; -.
InterPro; IPR006210; IEGF.
InterPro; IPR001368; TNFR_C6.
SMART; SM00181; EGF; 1.
SMART; SM00208; TNFR, 2.
PROSITE; PS50050; TNFR_NGFR_1; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUPERFAMILY MEMBER 18.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
BY SIMILARITY.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                     Name=C;
IsoId=O35714-3; Sequence=VSP_006511;
                                                                                                                                                                           IsoId=035714-2; Sequence=VSP_006510;
                                                                                                                                                        lsoId=035714-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
Migliorati G., Riccardi C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U82534; AAB81243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing.
SIGNAL 1 1
CHAIN 20 22
                                                                                                                                                                                                                                         lymphocytes.
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1754
1754
102
62
62
62
63
103
                                                                                                                                                                   Name=B;
                                                                                                                                              Name=A;
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TRANSMEM
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CARBOHYD
CARBOHYD
VARSPLIC
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REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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"Genome sequence of a human tumorigenic poxvirus: prediction of
specific host response-evasion genes.";
science 273:813-816(1996).

"C. -! - FUNCTION: ESSENTIAL FOR VIRAL REPLICATION. PLAYS AN IMPORTANT ROLE
DURING TRANSCRIPTION OF EARLY MRNAS, PRESUMABLY BY PREVENTING R-
LOOP FORMATION BEHIND THE ELONGATING RNA POLYMERASE. ACTS AS NTP-
DEPENDENT HELICASE THAT CATALYZES UNIDIRECTIONAL UNWINDING OF
3.TAILED DUPLEX RNAS. MIGHT ALSO PLAY A ROLE IN THE EXPORT OF
NEWLY SYNTHESIZED MRNA CHAINS OUT OF THE CORE INTO THE CYTOPLASM.

REQUIRED FOR PROPAGATION OF VIRAL PARTICLES (BY SIMILARITY).

C. -! - CATALYTIC ACTIVITY: NTP + H(2) 0 = NDP + phosphate.

C. -! - SIMILARITY: Belongs to the DEAD box helicase family. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 ö
                                               D/:
ETIG=VSP_006510.
ETQPFAEVQLSAEDACSFQFPEBERGEQTEEKCHLGGRWP
-> GQLCPREGENVSQAPHLPQFYYRDPAIRGGAVVS (in
isofoxm C).
/FTIG=VSP_006511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Locr-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nucleoside triphosphatase II (EC 3.6.1.15) (NTPase II) (Nucleoside triphosphatase II) (Nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96325459; PubMed=8670425;
Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                              1; Length 228;
                                                                                                                                                                                                                                                                                                                                                                    3; Indels
PCSPQQWRKWVYESGELRLGPMAAFLI
                                                                                                                                                                                                                           50D8C275D9C56259 CRC64;
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ATP-binding; Helicase; Hydrolase; Transcription.
DOMAIN 305 F20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           684 AA.
                                                                                                                                                                                                                                                                                              Score 39; DB .
Pred. No. 4.8;
2; Mismatches
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PIR, T30652; T30652.
InterPro; IPR001410; DEAD.
InterPro; IPR002464; DEAH box.
InterPro; IPR001650; Helicase C.
Pfam; PF00271; helicase C; 1.
SMART; SM00497; DEXDC; 1.
SMART; SM0490; HELICC; 1.
PROSITE; PS00690; DEAH_ATP_HELICAS
                                                                                                                                                                                                                                 228 AA; 25334 MW;
                                                                                                                                                                                                                                                                                           a 62.9%;
Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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receptor superfamily.";
Genomics 62:103-107(1999).
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                                                                                                                                                                                                    in vertebrates."
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TR19 MOUSE
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            STAR REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
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0
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV). Viruses; ssRNA negative-strand viruses; Mononegavirales; Rhabdoviridae; Novirhabdovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=89073771; PubMed=3201758;
Gilmore R.D. Jr., Leong J.C.;
"The nucleocapsid gene of infectious hematopoietic necrosis virus, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Conservative 1; Mismatches 0; Indels
                                                                                                                                                          Length 684;
                                                                                                                                                                                                                                           3; Indels
   ATP (BY SIMILARITY).
DEXH BOX.
51072BL93CC7284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 AA; 45700 MW; 5E2AFFF659BBEE38 CRC64;
                                                                                                                                                          Score 39; DB 1;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCAP IHNV STANDARD; PRT; 413 AA. P195691; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 01-MAY-1992 (Rel. 22, Last annotation update) Nucleocapsid protein (Nucleoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fish rhabdovirus.";
Virology 167:644-648(1988).
-!- PTM: Phosphorylated.
-!- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Per-hexamer repeat protein 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672 AA.
                                                                                                                                                                                                 Pred. No. 16;
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PIR; A31834; VHVNIH.
InterPro; IPR004902; Rhabdo_ncap_2.
Pfam; PF03216; Rhabdo_ncap_2; 1.
Nucleocapsid; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
   197 204 AT
308 311 DE
684 AA; 76556 MW;
                                                                                                                                                              62.9%;
                                                                                                                                                                                                 63.6%;
                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               CRPGLELREAG 127
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                                                                                                                                                                                                                                                                                                                     1 CRPGQELTKQG 11
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                    Local Similarity
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P08399;
NP_BIND
SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               117
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                                                                                                                                                          Query Match
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                                                                                                                                                                                                    Best Loc
Matches
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NCAP_IHNV
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SEQUENCE FROM N.A. (ISOFORM 4).
MEDLINE=20054362; PubMed=10585776;
Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
"Characterization of TNFRSF19, a novel member of tumor necrosis factor
                                                                                                 Shin H.S., Bargiello T.A., Clark B.T., Jackson F.R., Young M.W.; "An unusual coding sequence from a Drosophila clock gene is conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo, and Spleen;
MEDLINE-20270246; PubMed=10809768;

Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;

"TAJ, a novel member of the tumor necrosis factor receptor activates the c-Jun N-terminal kinase pathway and mediates caspase-independent cell death.";

J. Biol. Chem. 275:15336-15342(2000).
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Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Q9JLL3; Q9JHF1; Q9JJH6; Q9JLL2; Q9QXW7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 19 precursor (Toxicity and JNK inducer) (TRADE).
TNFRSF19 OR TROY OR TAJ.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 672;
                                                                                                                                                                                                     Nature 317:445-448 (1985).
-!- SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 672 G-T REPEATS.
672 AA; 57924 MW; E85BF428CF424C0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.3%; Score 38; DB 1; 77.8%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 3). TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M12039; AAA88320.1; -.
EMBL; X02966; CAA26710.2; -.
PIR; A24403; UMMS.
MGD; MGI:104521; Phxr5.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
SMART; SM00181; EGF; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
[1]
SEQUENCE FROM N.A.
MEDLINE=86014384; PubMed=2413365;
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Missing (in isoform 2).
/FTId=VSP 006514.
WSLRSQDIQYN -> CKLPSLCLTVK (in isoform
                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
T -> E (in isoform 2).
/FTId=VSP_006513.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 416;
Pred. No. 22;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   /FIId=VSP 006518

T -> A (IN REF. 1).

S -> P (IN REF. 1).

N -> D (IN REF. 3).

T -> A (IN REF. 3).

T -> A (IN REF. 3).
                                                                                                                                                                                   /FTId=VSP 006515.
Missing (In isoform 3).
/FTId=VSP 006516.
NESTASLDS -> MLCFRFRDL (in /FTId=VSP_006517.
                                                                                                                                                                                                                                                              Missing (in isoform 4)
/FTId=VSP_006518.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                       31 T T 208 S 287 N 343 T 45294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRPGOELTKO 10
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52 CGPGMELSKE 61
    106
114
1149
1105
150
                                                                                                                      416
                                                                                                                                                       214
                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                           416
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                                                                                                                                                                                                                                                                                                           31
208
287
343
416 AA;
     92
95
117
138
105
150
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                                                                                                                      151
                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
    DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
VARSPLIC
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                                                                                                                        /ARSPLIC
                                                                                                                                                         VARSPLIC
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TR19 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \stackrel{>}{\circ}
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                                                                                                    SECUENCE FROM N.A. (ISOFORM 1).

SECUENCE FROM N.A. (ISOFORM 1).

Chaudhary D., Long A.J.;

Chaudhary D., Long A.J.;

TRADE, a novel TNF receptor family member associated with death signaling.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

I. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Promote caspase-independent cell death (By similarity). Isoform 2 and isoform 3 may act as decoy receptors.

Chaudhary Database Swith TRAF1, TRAF2, TRAF3 and TRAF5 (By similarity).

Chaudhary DATABAS (By similarity).

Chaudhary DATABAS (By similarity).

Chaudhary DATABAS (By similarity).

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Chaudhary DATABAS (By similarity).

C
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                             receptor
    Senba E., Kitamura T.;
"TROY, a newly identified member of the tumor necrosis factor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles.";
J. Biol. Chem. 275:20742-20747(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 19.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (PARTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF173166; AAF19795.1; -.
EMBL; AF167552; AAF71825.1; -.
EMBL; AF167553; AAF71825.1; -.
EMBL; AB040432; BAB03267.1; -.
EMBL; AB040433; BAB03267.1; -.
EMBL; AB040433; BAB03268.1; -.
EMBL; AF247000; AAK28397.1; -.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6. 2.
SWART; SM00208; TNFR_C6. 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms=4;

Event-Alternative splicing; Named isoforms=4;

Event-Alternative splicing; Named isoforms=4;

Esoid=09JLL3-1; Sequence=Displayed;

Isoid=09JLL3-2; Sequence=VSP_005513; VSP_006514;

Name=3; Synonyms=TAJ-alphaS, dTROY;

Isoid=09JLL3-3; Sequence=VSP_006515, VSP_006516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
416
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Gaps

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TISSUE=Glial tumor;
MEDLINE=20347167; PubMed=10764796;
Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Senba E., Kitamura T.;
"TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles.";
Embryonic skin and hair follicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAF3 AND TRAFS.
TISSUE=Fetal spleen;
MEDLINE=20270246; PubMed=10809768;
Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
"TAJ, a novel member of the tumor necrosis factor receptor family, activates the c-Jun N-terminal kinase pathway and mediates caspase-independent cell death.";
J. Biol. Chem. 275:15336-15342(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2;
                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A. (ISOFORMS 1 AND 2).
Shaudhary D., Long A.J.;
"TRADE, a novel TNF receptor family member associated with death signaling.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
TR19 HUMAN STANDARD; PRT; 423 AA.
Q9NSG8; Q9BXZ9; Q9BYO0; Q9NZV2;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor receptor superfamily member 19 precursor (Toxicity and JNK inducer) (TRADE).
TNFRSF19 OR TROY OR TAJ.
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NCBI_TaxID=8090;
                                    DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
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DISULFID
CARBOHYD
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CONFLICT
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CONFLICT
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SEQUENCE
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                       RANGENER FROM N.A. LEGUTONER 2).

RA MIDINE=22388257; PubMed=12477932;

RA Strauberer R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Atlachul S. F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Zotdan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Bopaten M.J., Uddin T.B., Toshiyaki S., Carrinci P., Scheefer T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyaki S., Carrinci P., Prange C.
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Galmarathe P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ginarathe P.H.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Ginarathe P.H.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Ginarathe P.H.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Ginarathe P.H.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Ginarathe P.H.,
RA Bosak S.A., McWan P.J., McKernan K.J., Mare R.M., Gav L.J., Hulyk S.W.,
RA Mitliadon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mitliadon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Geren E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.,
RA Generation and initial analysis of more than 15,000 full-length
R. Proc. Nall. Acad. Sci. U.S.A. 99:16899-16933(2002).
C. TOURINT: Associates with TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, STONGASE L., Sequence—independent cell death.
C. SUBUNIT: Associates with TRARI, TRARI, TRARI, TRARI, STONGASE L., Sequence—independent
C. SUBUNIT: Associates with TRARI, TRARI, TRARI, TRARI, STONGASE L., Sequence—independent cell death.
C. SUBUNIT: Associates with TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARI, TRARIA TRABIA TRABEALA Laphane L. Sequence—Seed in prostate. Detected at
C. Subunyas=TRADEDeta; Sequence—Seed in prostate.
C. Noore-Rower Pevels in thymus Spiece, Lesselse in pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00652; TNFR NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR 2; 1.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM, 606122; -.
GO, GO:0016021; C:integral to membrane; NAS.
GO, GO:0005031; F:tumor necrosis factor receptor activity; NAS.
GO, GO:0006917; P:induction of apoptosis; NAS.
GO; GO:0007254; P:JNK cascade; NAS.
InterPro; IPR001368; TNFR_c6.
Pfam: PF00020; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
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 [4]
SEQUENCE FROM N.A. (ISOFORM 2)
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EMBL; AB040434; BAB03269.1; -.
EMBL; AF246998; AAK28395.1; -.
EMBL; AF246999; AAK28396.1; -.
EMBL; BC047321; AAH47321.1; -.
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191
423
72
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SIGNAL
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171
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SEQUENCE FROM N.A.

STRAIN-AA2, and HNI;

XX MEDLINE=21407746; PubMed=11516953;

RA Cato S., Kuwahara Y., Kondo M., Naruse K., Mitani H., Wakamatsu Y.,

RA Ozato K., Asakawa S., Shimizu N., Shima A.;

RT The medaka rs-3 locus required for scale development encodes

RT ectodysplasin-A receptor.";

RI Curr. Biol. 11:1202-1206(2001).

C. '-- FUNCTION: Receptor for EDA (By similarity). May mediate the

activation of NF-kappa-B and JNK.

C. '-- FUNCTION: Type I membrane protein (Probable).

C. '-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

C. '-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

C. '-- SUBCELLULAR COCATION: Type I membrane protein (Probable).

C. '-- SUBCELLULAR COCATION: Type I membrane protein (Probable).

C. '-- SUBCELLULAR COCATION: Type I membrane protein (Probable).

C. '-- SUBLIARITY: Contains 3 TNFR-Cys repeats.

C. '-- SIMILARITY: Contains 3 TNFR-Cys repeats.

C. '-- SIMILARITY: Contains 1 Todath domain.

C. '-- SIMILARITY: Contains 1 Todath domain.
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                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHORGEST -> EA (in isoform 2).
CHIGEVSP 006512.
S -> T (IN REF. 3; AAK28396).
T -> A (IN REF. 1).
GS -> ET (IN REF. 1).
GS -> ET (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDAR ORYLA STANDARD; PRT; 514 AA. 090VY2; 090Z36; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member EDAR precursor (Ectodysplasin-A receptor) (Reduced scale-3 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
O
                                                                                                                                                                                                                                                                                                                                                                            31 S -> T (IN REF. 3; AAK28396).
74 T -> A (IN REF. 1).
216 GS -> ET (IN REF. 1).
221 F -> L (IN REF. 3; AAK28396).
330 T -> A (IN REF. 3; AAK28396).
405 V -> I (IN REF. 3).
A, 46015 MW; B5891CEA9ED45361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Score 37; DB 1; Length 423; 60.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzias latipes (Medaka fish) (Japanese ricefish).
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1114
1499
622
722
1006
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1135
1233
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                                                                                                                                                                                                                                                                                                                                                                                 31
215
221
330
405
423 AA;
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